

## **FIGURE 1**

ACTGCACCTCGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA  
CCCACCGCGTCCGGGCCGGAGCAGCACGGCGCAGGACCTGGAGCTCCGGCTCGCTCTCCG  
CAGCGCTACCCGCCATCGCCTGCCGCCGGCCGCTGGGCTCCTGCCGCTTCTGCTG  
CTGCTGCCGCCGCCGGAGGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGCT  
GGTGGACAAGTTAACCAAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCCGGAAACA  
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCTGCTGGAGATC  
CTGGAGGGCTGTGCGAGAGCAGCAGTCGAATGCAATCAGATGCTAGAGGCCAGGAGGA  
GCACCTGGAGGCCTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCAGTGTCTCGCATGC  
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGGAGATGGGAGCAGACA  
CGCACGGGTCCCTGCCGGTGCCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG  
GGCTACTTCAGCTCGCTCCGAAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC  
AAAGACGTGCTCGGCCTGACCAACAGAGACTGCGCGAGTGTGAAGTGGCTGGGTGCT  
CGAGGGCGCCTGTGGATGTGGACAGTGTGCGGCCAGCCGCTCCCTGCAGCGCTG  
AGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTACTCCAGCTGTG  
TGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCCAGGGAGCA  
ACAGTGTGAGATGTGGACGGAGTGCTCACTAGCAGAAAAACCTGTGTGAGGAAAAACG  
ACTGCTACAATACTCCAGGGAGCTACGTCTGTGTCTGACGGCTTCGAAGAAACG  
GATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCACACAGCT  
CTCCCGCAAGACCTGTAAATGTGCCGACTTACCTTAAATTATTAGAAGGATGTCC  
GAAAATGTGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGCCGGGAGAGGCTGC  
CTCTCTAACGGTTGATTCTCATTTGTCCTAAACAGCTGCATTCTGGTTGTTCTTA  
AGACTTGTATATTTGATAACAGTTCTTGTAATAAAATTGACCATTGTAGGTAATCAGG  
AAAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAGAAC  
CCGCCATGGCCAACTTGTTATTGCAGCTATAATGGTTACAAATAAGCAATAGCA  
CACAAATTTCACAAATAAGCATTTCACTGCATTCTAGTTGTGGTTGCTCAAAC  
ATCAATGTATCTTATCATGTCTGGATCGGAATTAATCGGCCAGCACCATGCCCTGAAAT  
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTCTGAGGCCAGAACCCAGCTGTGGAATG  
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAACAGTATGCAAGCATGC  
ATCTCAATTAGTCAGCAACCCAGTTT

## **FIGURE 2**

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pi: 4.53, NX(S/T): 2

MRLPRRAALGLPLLLLPPAPEAAKKPTPCHRCGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL  
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLCVCCSPGTYGPDCLACQGGSQRPCSG  
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHSICTACDESCKTCGLTNRDCGECEVGWLDE  
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDEC SLAEKT  
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

**Signal peptide:**

amino acids 1-24

**N-glycosylation sites.**

amino acids 190-194 and 251-255

**Glycosaminoglycan attachment sites.**

amino acids 149-153 and 155-159

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 26-30

**Casein kinase II phosphorylation sites.**

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343  
and 349-353

**Tyrosine kinase phosphorylation site.**

amino acids 303-310

**N-myristoylation sites.**

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and  
313-319

**Aspartic acid and asparagine hydroxylation site.**

amino acids 308-320

**EGF-like domain cysteine pattern signature.**

amino acids 166-178

**Leucine zipper pattern.**

amino acids 94-116

## **FIGURE 3**

CAGGTCCAAC TGCACCTCGGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTC  
GACCTCGACCCACCGCGTCCGCCAGGCCGGAGGCAGCGGCCAGCCGTCTAACGGGAACA  
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG  
GCACCGAGGAGTTTCCCGGCAGCGAGGAGGTCTGAGCAGCAGATGGCCCGGAGGAGGCCCTTC  
CCTGCCGCCCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCCGGCGGAGGC  
CGGGCCGCCGCAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAAGGCAAGAGTACTCA  
TAGGATTGAGAAGATATCCTGATTGTTCAGAGGGAAAATGGCACCTTACACATGAT  
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTCAC  
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGTCCCTGCCTCCCTGGATA  
AAGGCATCATGGCAGATCCAACCGTCAATGTCCTCTGCTGGAAACAGTGCCTCACAGGCA  
TCAGTTGTTCAAGTTGTTCCATGTCTGGAAAACAGGATGGGTGGCAGCATTGAAGT  
GGATGTTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAATGCTATCT  
TCTTAAAACATGTCAACAAGCTGAGTGCCAGGCCGGTGGCAAATGGAGGCTTTGTAAT  
GAAAGACGCATCTCGAGTGTCTGATGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG  
TACCCCACGATGTATGAATGGTGGACTTGTGTGACTCCTGGTTCTGCATCTGCCACCTG  
GATTCTATGGAGTGAAC TGTGACA AAGCAA ACTGCTCAACCACCTGCTTAA TGGAGGGACC  
TGTTCTACCTGGAAAATGTATTGCCCCTCAGGACTAGAGGGAGAGCAGTGTGAAATCAG  
CAAATGCCCAACCCGTGAAATGGAGGTAAATGCAATTGGTAAAGCAAATGTAAGTGT  
CCAAAGGTTACCAGGGAGACCTGTTCAAAGCCTGTCTGCAGCCTGGCTGGTGACAT  
GGAACCTGCCATGAACCCAACAAATGCCATGTCAAGAAGGTTGGCATGGAAGACACTGCAA  
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCCAGCTCAGGCAGC  
ACACGCCCTCACTAAAAAGGCCAGGAGCGGGATCCACCTGAATCCAATTACATCTGG  
TGAAC TCCGACATCTGAAACGTTTAAGTTACACCAAGTTACAGCCTTGTAAACCTTCA  
TGTGTTGAATGTTCAAATAATGTTCAATTACACTTAAGAATACTGGCCTGAATT TATTAGCT  
TCATTATAAATCACTGAGCTGATATTACTCTTCTTTAAGTTCTAAGTACGTCTGTAG  
CATGATGGTATAGATTCTTGTTCAGTGCTTGGACAGATTATATTATGTCAATTGA  
TCAGGTTAAAATTTCAGTGTAGTTGGCAGATATTCTCAAATTACAATGCATTATGGT  
GTCTGGGGCAGGGAACATCAGAAAGGTTAAATTGGCAAAATGCGTAAGTCACAAGAAT  
TTGGATGGTGAGTTAATGTTGAAGTTACAGCATTCAAGATTATTGTCAAGTATTAGAT  
GTTGTTACATTAAAATTGCTCTTAATTAAACTCTCAATAACATATATTGACC  
TTACCAATTCCAGAGATTCACTATTAAAAAAATTACACTGTGGTAGTGGCATT  
AAACAAATATAATATTCTAAACACAATGAAATAGGAAATATAATGTATGAACCTTGCAT  
TGGCTTGAAGCAATATAATATTGTAACAAACACAGCTCTTACCTAATAAACATTAT  
ACTGTTGTATGTATAAAATAAGGTGCTGCTTAGTTTTGGAAAAAAA  
AAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCACCTGCAGAAGCTTGGC  
CGCCATGGCCCAACTGTTATTGCAGCTTATAATG

## **FIGURE 4**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPCEKALCTPRCMNGLCVTPGFCICPPGFYGVNCDKANCST
TCFNNGGTCFYPGKCI CPPGLEGEQCEISKCPQPCRNGGKCI GKSCKCSKGYQGDLCSPV
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW
```

**Signal peptide:**

amino acids 1-28

**N-glycosylation site.**

amino acids 88-92, 245-249

**Casein kinase II phosphorylation site.**

amino acids 319-323

**Tyrosine kinase phosphorylation site.**

amino acids 370-378

**N-myristoylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

**EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

## **FIGURE 5**

CGGACGCGTGGCGTCCGGCGTCGAGAGCCAGGAGGCGCGCGGGCCAGCCTGGG  
CCCCAGCCCACACCTCACCAAGGGCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTAC  
TGCTGTTGCTGCCGCTGGCTGCCACTGGCTCTGGGTGCCAGCAGGGTGTGGCGCCGG  
GAGCTAGCACCGGTCTGCACCTGCCGGCATCCGGACGGGGAGGCCGGTACTGCCAGGA  
GCAGGACCTGTGCTGCCGCGGCCGTGCCAGCAGACTGTGCCCTGCCCTACCTGGCGCCATCT  
GTTACTGTGACCTCTCTGCAACCGCACGGTCTCGACTGCTGCCCTGACTCTGGGACTTC  
TGCCTCGGCGTGCCACCCCTTTCCCCGATCCAAGGATGTATGCATGGAGGTGTATCTA  
TCCAGTCTTGGGAACGTACTGGGACAACGTGAACCGTTGCACCTGCCAGGAGAACAGGCAGT  
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG  
GAACACAGCGCCTCTGGGCATGACCTGGATGAGGGATTGCTACCGCCTGGCACCA  
TCCGCCCACCTTCCTCGTCATGAACATGATGAAATTATACAGTGTGAACCCAGGGAG  
GTGCTTCCCACAGCCTCGAGGCCTCTGAGAACGAGCTGGCCAAACCTGATTGATGAGCCTTGA  
CCAAGGCAACTGTGCAGGCTCTGGGCCTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT  
CAATCCATTCTCTGGACACATGACGCCGTCTGTCGCCCCAGAACCTGCTGTCTTGAC  
ACCCACCAGCAGCAGGGCTGCCCGTGGCGTCTCGATGGTGCCTGGTGGTTCTGCGTCG  
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTCTGGGCCGTGAACGAGACGAGGCTGGCC  
CTGCGCCCCCTGTATGATGACAGCCGACATGGGTGGGGCAAGGCCAGGCCACTGCC  
CACTGCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGCTACCGCCT  
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAACGGCCCTGTCCAAGCCCTCA  
TGGAGGTGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGC  
CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG  
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCCAACCTCTGGGCC  
CAGCCTGGGCGAGAGGGCCACTTCCGATCGCGCGCTCAATGAGTGCACATCGAG  
AGCTTCGTGCTGGCGCTGGGCCGCGTGGCATGGAGGACATGGGTATCACTGAGGCTG  
CGGGCACACCGCGGGTCCGGCTGGATCCAGGCTAACGGCCGGCGGAAGAGGCCCAATG  
GGCGGTGACCCAGCCTGCCGACAGAGCCGGCGCAGGCCGGCGCCAGGGCGCTAA  
CCGGCGCGGGTCCGCTGACCGAGCAGCCCGCCTGGAGGCCGGCAGGGAGACTGGCG  
GAGCCCCCAGACCTCCCAGTGGGACGGGCAGGGCTGGCCTGGGAAGAGCACAGCTGCAG  
ATCCCAGGCTCTGGGCCCAACTCAAGACTACCAAAAGCCAGGACACCTCAAGTCTCCAGC  
CCCAATACCCACCCAAATCCGTATTCTTTTTTTTTAGACAGGGCTTGTCCG  
TTGCCAGGTGGAGTGCAGTGGCCATCAGGGCTCACTGTAACCTCCGACTCTGGTTCA  
AGTGACCTCCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCACACCTGGC  
TAATTTTGATTTTGTAAGAGGGGGTCTCACTGTGTGCCCAGGCTGGTTCAACT  
CCTGGCTCAAGCGGTCCACCTGCCCTCCCAAAGTGCTGGATTGCAGGCATGAGCC  
ACTGCACCCAGCCCTGTATTCTATTCTCAGATATTATTTCTTCACTGTTAAAAA  
TAAAACCAAAGTATTGATAAAAAAAA

## **FIGURE 6**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAAGGRYEQDLCCRGRADDC
ALPYLGAICYCSDLFCNRTVSDCCPDFWDFCLGVPPPFPPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEQRLLGHDPG
```

**N-glycosylation site.**

amino acids 78-82, 161-165

**Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

**N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

**Amidation site.**

amino acids 26-30, 318-322

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

## **FIGURE 7**

AGGCTCCTGGCCCTTTCCACAGCAAGCTNTGCNATCCGATTGTTGCTCAAATCCA  
ATTCTCTTGGGACACATNACGCCCTGTCCTTNGCCCCAGAACCTGCTGTCTGTACACCCAC  
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTCCCTGCCGTGCCGAGG  
GNTGGTGTCTGACCACTGCTACCCCTCTCGGCCGTGAACGAGACGAGGCTGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGGTGGGGCAAGGCCAGGCCACTGCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGTCTACCGCCTGGCTC  
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGCCCTGTCCAAGCCCTATGGAGG  
TGCATGAGGACTTCTTCCATACAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTGGG  
AGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAG

## **FIGURE 8**

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG  
GAGCAGTGCTGGACCGCGCGCATCCGCCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG  
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT  
GCGCTGCTCCCTGCACTCGGCCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG  
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG  
GCCCACTGGGAGCCTGTCCTGGTTCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT  
CTGCACCCCTGTCCCCCACCTGACCCCTCCATGCCCTCTCCAGGACTCCACCCGGCAGA  
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGCCCTCCAACCCCTCTGCTGCTGTTTC  
CATGGCCCAGCATTCTCCACCCCTAACCCCTGTGCTCAGGCACCTCTCCCCCAGGAAGCCTT  
CCCTGCCACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA  
GGGGACAGGCACTCAGGAGGGCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA  
GGACAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGCCTGGAGGCCTGGAGGAA  
GGGCCAGGCCACATTGTTGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT  
AATAAACACCTGTTGGATAAGCCAAAAAA

## **FIGURE 9**

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSLDT  
DPPADGPSNPLCCCFHGPASFILNPVLRHLFPQEAFPAHPIYDLSQVWSVSPAPSRGQALRRAQ

**Signal peptide:**

amino acids 1-47

**N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

**Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

**N-myristoylation site.**

amino acids 56-60

**Amidation site.**

amino acids 70-74

## **FIGURE 10**

CCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCGCTGCTGCCAACCTCACTCTGT  
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGCGCCATGACC  
GACCAGCTGAGCAGGCCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTCAGGTACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC  
TCATAGTGGAGACGGACACGTTGGCAGCCGGGTTCGCATCAAAGGGCTGAGAGTGAGAAG  
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGAAGAGCAAAGACTG  
CGTGGTTCATGGCCTTCACGCCAGGGCGGCCAGGCTCCGCAGGCCAGAAC  
CAGCGCGAGGCCACTTCATCAAGGCCCTACCAAGGCCAGCTGCCCTCCCCAACACGC  
CGAGAACAGAACAGTCGAGTTGTGGCTCCGCCACCCGCCGGACCAAGCGCACAC  
GGCGGCCAGGCCCTCACGTAGTCTGGGAGGCAGGGGCAGCAGCCCTGGGCCCTCCC  
CACCCCTTCCCTTCAATCCAAGGACTGGCTGGGTGGCGGGAGGGAGGCCAGATCCCC  
GAGGGAGGACCTGAGGCCCGAAGCATCCGAGCCCCAGCTGGGAAGGGCAGGCCGGTG  
CCCCAGGGCGGCTGGCACAGTCCCCCTCCCGACGGTGGCAGGCCCTGGAGAGGAAC  
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCCTGAAGCC  
CGCTGAAAGGTCAAGCGACTGAAGGCCTTGCAGACAACCGTCTGGAGGTGGCTGTCTCAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGGCCCCAAACTCCTCCTGGCTAGACTGTA  
GGAAGGGACTTTGTTGTTGTTGTTCAGGAAAAAAGAAAGGGAGAGAGAGGAAATAG  
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCCAACTCCAGCCC  
CGGAATAAAACCATTTCCTGC

## **FIGURE 11**

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI  
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKDCVFTEIVLE  
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF  
VGSAPTRRTKRTRRPQPLT

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 9-13, 126-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

**Casein kinase II phosphorylation site.**

amino acids 65-69

**Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

**N-myristoylation site.**

amino acids 69-75, 188-194

**Amidation site.**

amino acids 58-62

**HBGF/FGF family signature.**

amino acids 103-128

## **FIGURE 12**

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTCATGGAG  
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC  
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTCTGGACTTCAACAGAACCCCATCCAGT  
CATTTGATTGCTGTTATTTCCTTTCTTTCCCACCATTTGATTATTTAT  
TTCCGTACTCAGAAATGGGCTACAGACCACAAAGTGGCCAGCCATGGGCTTTTCCT  
GAAGTCTTGGCTTATCATTCCCTGGGCTACTCACAGGTGTCAAACCTCTGGCTG  
CTAGTGTGTGCCGCTGCGACAGGAACCTTGCTACTGTAATGAGCGAAGCTGACCTCAGTG  
CCTCTGGATCCCAGGGCTAACCGTACTCTACCTCCACAACAACAAATTATAATGC  
TGGATTTCCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC  
AACTGGACGAATTCCCCATGAACCTTCCAAGAATGTCAAGGTTCTCCATTGCAAGGAAAC  
AATATTCAAGACCATTCACGGCTGCTTGCCCCAGCTCTGAAGGTTGAAGAGCTGCACCT  
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCTTCCGGAGGCTATTAGCC  
TCAAATTGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCCCTGGCTTCCGTGGAC  
TTGCAAGAGCTGAGAGTGGATGAAATCGAATTGCTGTATCCGACATGCCCTCCAGAA  
TCTCACGAGCTGGAGCGTCTATTGTTGACGGGAACCTCTGACCAACAAGGGTATGCCG  
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATTGTAATTGCAATTGCTGTCC  
CACCCCTCCCTCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAAGGACAACCAAGAT  
AAACACATCCCTTGACAGCCTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA  
ACAACCAACTGCGGATGCTGACTCAAGGGTTTGATAATTCTCCAACCTGAAGCAGCTC  
ACTGCTCGGAATAACCTTGGTTTGACTGCAGTTAAATGGGTACAGAATGGCTCAA  
ATATATCCCTCATCTCAACGTGCGGGTTCATGTGCCAAGGTCTGAACAAGTCCGGG  
GGATGGCCGTCAAGGAATTAAATATGAATCTTGTCCCTGCTCCACCACGACCCCCGGCCTG  
CCTCTCTTACCCCAGCCCCAAGTACAGCTCTCGACCCTCAGCCTCCACCCCTCTCTAT  
TCCAAACCCTAGCAGAAGCTACACGCCTCCAACCTTACCCACATCGAAACTTCCCACGATT  
CTGACTGGGATGGCAGAGAAAGAGTGACCCCCACCTATTCTGAACGGATCCAGCTCTATC  
CATTGTTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTTCAACCGTGTGGCATA  
CAAACACTCACATGGGTGAAATGGGCCACAGTTAGTAGGGGGCATCGTTAGGAGCGCATAG  
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT  
TGTGTTAGTGCCACTGGATGCTTTAACTACCGCGCGGTAGAAGACACCATTGTTAGGAGGC  
CACCAACCATGCCTCTATCTGAACACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGATGGGGCGCGGTGATATT  
GTGCTGGTGGCTTGCTCAGCGTCTTGCTGGCATATGCACAAAAGGGCGCTACACCTC  
CCAGAAGTGGAAATACAACCGGGCCGGAAAGATGATTATTGGAGGCAGGCACCAAGA  
AGGACAACCTCCATCTGGAGATGACAGAAACCAGTTTCAGATCGTCTCTTAAATAACGAT  
CAACTCCTTAAAGGAGATTTCAGACTGCAGCCATTACACCCCAAATGGGGCATTAATTA  
CACAGACTGCCATATCCCCAACAAACATGCGATACTGCAACAGCAGCGTGCAGACCTGGAGC  
ACTGCCATACGTGAAGCCAGAGGCCAGCGTTATCAAGCGGACAATTAGACTCTTGAGAA  
CACACTCGTGTGACATAAAGACACGCAGATTACATTGATAATGTTACACAGATGCAT  
TTGTGCATTGAATACTCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAGTG  
CTATCTTCTATTCAAGTTAATTACAAACAGTTTGTAACTCTTGCTTTAAATCTT

## **FIGURE 13**

MGLQTTKWPShGAFFLKSLLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP  
EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI  
SRAALAQLLKLEELHLDNSISTVGVEDGAFREAISLKLFLSKNHLSSVPVGLPVDLQELR  
VDENRIAVISDMAFQNLTSLERLIVDGNNLLTNKIAEGTFSHLTKLKEFSIVRNSLSHPPPD  
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN  
PWFCDCSIKWVTEWLKYIPSSLNVRGFMQCQGPEQVRGMAVRELMNLLSCPTTPGLPLFTP  
APSTASPTTQPPTLSIPNPSRSYTPPPTTSLPTIPDWDGRERVTPISERIQLSIHFVND  
TSIQVSWLSLFTVMAYKLTWVKGHSIVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL  
DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL  
LSVFCWHMHKKGRYTSQWKYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG  
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

## FIGURE 14

ACTTGGAGCAAGCGGCGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGCTCCGTCCGCCCTCCACGAGCG  
ATCCCCGAGGAGAGCCGCGGCCCTCGGCCAGGGCGAAGAGGCCAGAGGAAGACCCGGGTGGCTGCCCTGCC  
TCGCTTCCCAGGCAGGCCCTCGCAGGCCCTTGCTGCCCTTGCTGCCCTGAAATGGAAAAGATGCTCGCAGGCT  
GCTTCTGCTGATCCTCGGACAGATCGCCTCCCTGCCAGGGCAGGGAGCGGTACGTGGAGGTCCATCT  
CTAGGGGCAGACAGCTCGGACCCGAGACGGCCCTCTGGAGAGTTCTGTGAGAACAGCAGGGCAGACC  
TGGTTTCATCATTGACAGCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTGGACA  
TCTTCAATTGGACATTGGCCTGTGTCAGTGTCAACACCCATGCTTCAAGAGGATGCGACTGTCAAGAATG  
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCGTGTCAAGAGGATGCGCATCTGTCACGG  
GCACCATGACTGGCTGGCCATCCAGTATGCCCTGAAACATCGCATTCTCAGAAGCAGAGGGGCCGGCCCTGA  
GGGAGAATGTGCCACGGTCTATAATGATCGTACAGATGGAGACCTCAGGACTCCGTGGCCAGGGTGGCTGCTA  
AGGCACGGGACACGGGATCCTAACTTGCCTGGCAATTGGTGGCCAGGTAGACTTCAACACCTGAAAGTCCATTG  
GGAGTGAGCCCCATGAGGACCATGTCCTTGTGGCAATTTCAGCCAGATTGAGACGCTGACCTCCGTTC  
AGAAGAAGTTGTGACGGCCCACATGTGAGCAGCACCTGGAGCATAACTGTGCCACTTCTGCATCAACATCCCTG  
GCTCATACGTCTGCAGGTCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCGAGAATCCAGGATCTGT  
GTGCCATGGAGGACCACAACGTGAGCAGCTGTGTAATGTGCCCTGGCTCTTCGTCAGTGTACAGTG  
GCTACGCCCTGGCTGAGGATGGAGAGGTGTGGCTGGACTACTGTGCCCTAGAAAACCACGGATGTGAAC  
ATGAGTGTAATGCTGATGGCTCTACCTTGCCAGTGCATGAAGGATTGCTCTTAACCCAGATGAAAAAA  
CGTGCACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCGTCAAACATGGAGGAGAGCT  
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGAAAACCTGCAAGCCGAGTGGACACTGTGCAC  
AGCAGGACCATGGCTGTGAGCAGCTGTGTAACACCGAGGATTCCCTCGTCGCACTGCTCAGAAGGCTTC  
TCATCAACGAGGACCTCAAGACCTGCTCCGGGTGGATTACTGCCTGCTGAGTGACCATGGTTGTGAATACTCCT  
GTGTCACATGGACAGATCCTTGCCCTGTCAGTGTCTGAGGGACACGTGCTCCGAGCGATGGGAAGACGTGT  
CAAAATTGGACTCTTGTGCTCTGGGGACCACGGTTGTGAACATTGCTGTGTAAGCAGTGTGCAAGCTATAG  
GCCAGTGCTTGAAGGTTATATACTCCGTGAAGATGGAAAACCTGCAAGAGAAAGATGCTGCCAAGCTATAG  
ACCATGGCTGTGAACACATTGTGTAACAGTGACACTACACGTGCGAGTGTGGAGGGATTCCGGCTCG  
CTGAGGATGGAAACGGCTGCCAGGGAGGATGCTGCAAATCAACCCACCATGGCTGCGAACACATTGTGTTA  
ATAATGGGAATCCTACATCTGCAAATGCTCAGAGGGATTGTTCTAGCTGAGGACGGAAGACGGTGCAAGAAAT  
GCACTGAAGGCCAATTGACCTGGCTTGCTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAATTGAGGTGCG  
TGAAGCAGTTGTCACTGGAATTATAGATTCCCTGACAATTCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGT  
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTTCAACTCAGCCAAAGACATGAAAAAGCCGTGGCCC  
ACATGAAATACATGGAAAGGGCTTATGACTGGCTGGCCCTGAAACACATGTTGAGAGAAGTTTACCAAG  
GAGAAGGGGCCAGGCCCTTCCACAAGGGTGCCAGAGCAGCCATTGTTGTCACCGACGGACGGCTCAGGATG  
ACGTCCTCGAGTGGGCCAGTAAAGCCAAGGCCATGGTACTATGCTGTTGGGGTAGGAAAAGCCATTG  
AGGAGGAACATACAAGAGATTGCTCTGAGCCCACAAACAGCATCTTCTATGCCGAAGACTCAGCACAATGG  
ATGAGATAAGTAAAAACTCAAGAAAGCATTGTGAGAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG  
CAGGGGAACCTGCAAAACGGTCAACAGCAACAGAAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT  
CCTGTTCTAATTGCACTGCAACACAGATATCTGTTGAAGAAGACAATCTTACGGCTCACACAAAAGCTT  
CCCATTCAACAAAACCTCAGGAAGGCCCTTGAAGAAAACAGCATCAATGCAAATGTGAAAACCTTATAATGT  
TCCAGAACCTTGCACAGAAGAAGTAAGAAAATTAAACACAGCGTTAGAAGAAAATGACACAGAGAATGGAAGGCC  
TGGAAAATCGCTGAGATACAGATGAAGATTGAAATCGGCACACATTGTTAGTCATTGTATCACGGATTACAAT  
GAACGCAGTGCAGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTAAGTAAACAAATCAGTACTGA  
GAAACCTGGTTGCCACAGAACAAAGACAAGAGAATGAAATAAGCTATGCAAGGTATTGTTGAAATATACTGTGGACAC  
TCAGAATTCTAAGATGAATTACAGGTGAGAATGAAATAAGCTATGCAAGGTATTGTTGAAATATACTGTGGACAC  
AACTTGCTCTGCCTCATCTGCCTAGTGTGCAATCTCATTGACTATACGATAAAAGTTGCACAGTCTTACTT  
CTGAGAACACTGCCATAGGAAATGCTGTTTTTGACTGGACTTACCTGATATATGTATATGGATGTATG  
CATAAAATCATAGGACATATGTACTTGTGGAACAAGTTGATTAAATTTACAAATATTAAATTCAACACTTCAG

## **FIGURE 15**

MEKMLAGCFLLILGQIVLLPAEARERSGRSISRGRHARTHPTALLESSCENKRADLVII  
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV  
KRMRLSTGTMGLAIQYALNIAFSEAEGRPLRENVPRVIMIVTDGRPQDSVAEVAAKARD  
TGILIFAIVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVQKKLCTAHMCSTLEHN  
CAHFCINIPGSYVCRKQGYILNSDQTTCTRIQDLCAMEDHNCEQLCVNPGSFVCQCYSGYA  
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKGPC  
EHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI  
NEDLKTCSRVDYCLLSDHGCEYCVNMDRSFACQCPEGHVLRSRGKTCAKLDSCALGDHGCE  
HSCVSSEDSFVCQCFCGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRILA  
EDGKRCRKKDVCKSTHHGCEHICVNNNGNSYICKCSEGFVLAEDGRRCKCTEGPIDLVFVID  
GSKSLGEENFEVVKQFVTGIIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA  
HMKYMGKGSMTGLALKHMFERSFTQGE GARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN  
GITMYAVGVGKAIEELQEIASEPTNKHLYAEDFSTMDEISEKLKGICEALEDSDGRQDS  
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLHSTKPSGPL  
EEKHDQCKCENLIMFQNLANEVRKLTQRLEEMTQRMEALENRLRYR

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

**Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,  
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,  
781-785, 819-823, 866-870

**N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,  
639-645, 690-696, 752-758, 792-798

**Amidation site.**

amino acids 314-318, 560-564, 601-605

**Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,  
540-546, 581-587

## **FIGURE 16**

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCGTCGCGCAGCCTCG  
GCACCTGCAGGTCCGTGCGTCCCGGGCTGGCGCCCTGACTCCGTCCGGCCAGGGAGGGC  
**CATGATTCCCTCCGGGCCCCCTGGTACCAACTTGCTGCGGTTTTGTTCTGGGCTGA**  
GTGCCCTCGGCCCTCGCGGGCCAGCTGCAACTGCACCTGCCGCCAACGGTTGCAG  
GCGGTGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGAGGTGTCTTC  
ATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGTCCTACATCAATGGGTACAAACAAGCAAACCTGGAGTATCCTGGTCTACTCC  
ATGCCCTCCCGAACCTGTCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATAAAACCT  
TAGAACTCAATGTAATGGTTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT  
GTGGGGCAAACGTGACCTGAGCTGCCAGTCTCAAGGAGTAAGCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTTCCATCCTCCAGACTTCTTGCACCAAGCATTAGATGTCATCCGTG  
GGTCTTAAGCCTACCAACCTTCGTCTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC  
AATGAGGTGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGCCCTGGAGCTGC  
AGTGGTTGCTGGAGCTGTTGGTACCTGGTTGGACTGGGTTGCTGGCTGGCTGGTCC  
TCTTGTACCAACGCCGGCAAGGCCCTGGAGGAGCCAGCAATGATATCAAGGAGGATGCC  
ATTGCTCCCCGGACCTGCCCTGGCCAAGAGCTCAGACACAATCTCAAGAATGGGACCC  
TTCCTCTGTACCTCCGCACGAGCCCTCCGCCACCCATGGCCCTCCCAGGCCTGGTGCAT  
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGAT  
GGGGCCACCCCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG  
CATGGGTGCTGTCCTGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTAT**GATGAC**  
CCCACCACTCATGGCTAAAGGATTGGGCTCTCCTCTATAAGGGTCAACCTCTAGCAC  
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCGACCCCTAGTACTCTGCCACCTCTC  
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCTTATGAAGCCAGCTG  
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTCAAGTCTCCAGGC  
CCCCTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCGT  
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTACTGGGCAGAGGATAGGAAATCTC  
TTATTAACATGAAATATGTGTTTTCTTGCAAATTAAATAAGATACATAA  
**TGTTGTATGAAAAA**

## **FIGURE 17**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLP AWYTLHGEVSS  
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEG LQEKD SGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHGANVTLSCQSPRSKPAVQYQ  
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGT AQC NVTLEVSTGPGAA  
VVAGAVVGT LVGLGLLAGLVLLYHRRGKALEEPANDIKA DAIAPRTL PWPKSSDTISKNGTL  
SSVTSARALRPPHGPPRPGALTPPSLSSQALPS PRLPTTDGAHPQPISPIPGGVSSSGLSR  
MGAVPVMVPAQSQAGSLV

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 245-267

**N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

**N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

## **FIGURE 18**

## **FIGURE 19**

MKRLPLLVVFSTLLNCYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC  
GNLTQSCGENANCTNTEGSYYCMCVPGRSSSNQDRFITNDGTVCIENVANCHLDNVCIAA  
NINKTLTKIRSIKEPVALLQEVEYRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL  
SNSTLTFVKTVNNFVQRDTFVWDKLSVNHRRTLTKLMHTVEQATLRISQSFKTTEFDT  
NSTDIALKVFFFDSYNMKHIHPHMNMDGYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS  
SSDNFLLKPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAF  
WNYSPDTMNGWSSEGCELTYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLG  
IIISLICLAI CIFTWFFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCIIAGL  
LHYFFLAAFAWMCIEGIHLYLIVGVVIYNKGFLHKNFYIFGYLSPAVVVGFSAA LGYRYYGT  
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGVLHVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV  
PCCFGCLR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,  
648-664

**N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

**Glycosaminoglycan attachment site.**

amino acids 49-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

**Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

**Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

**N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

**Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

## **FIGURE 20**

TGGAAACATATCCTCCCTCATATGAATAATGGATGGAGACTACATAAATATATTCCAAAGNG  
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT  
TGGTCCCTTGCTTTCATCATCTGACAACCTTCTATTGAAACCTCAAAATTATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCACTGAGCTCAAACCCACCCAC  
ATTATATGAACTTGAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA  
GGAGTCTATGTGGCATTGGAAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTGCAATTGATGTCCTGGTCCTCCATTGGTATTAAAGATTATAATATTCTTACAA  
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTTACCTTC  
TGGTTCTTCAGTGAATTCAAAGCACCAGGA

## **FIGURE 21**

GCTCCAGCCAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGGAGTTCCCCGAAACCCGGCCG  
CTAAGCGAGGCCCTCCTCCCGCAGATCCGAAACGCCCTGGCGGGGTCACCCCGGCTGGGA  
CAAGAAGCCGCCCTGCCCTGCCCCGGGGAGGGGGCTGGGCTGGGGCTGGGCCGGAGGC  
GGTGTAGTGGGTGTGCGGGGGCGGAGGCTTGATGCAATCCGATAAGAAATGCTCGG  
TGTCTGGGCACCTACCGTGGGCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG  
CCGCCGCCGTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCACGACCATCCAAACCC  
GGCACTCACAGCCCCGAGCGCATCCGGTCGCCGCCAGCCTCCGCACCCCCATGCCGG  
AGCTGCGCCAGAGCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTTGGTCCACGTATGG  
ATCCTGGCCGGCTCTGGCTGGCGGCCCCCTGCCTTCTCGGACGCCGGCC  
CCACGTGCACTACGGCTGGGCGACCCCATCCGCCTGCGCACCTGTACACCTCCGGCCCC  
ACGGGCTCTCCAGCTGCTTGCATCCGTGCCGACGGCGTGTGGACTGCCGCCGG  
CAGAGCGCAGCTTGTGGAGATCAAGGCAGTCGCTCTGCCGACGGCAAGATGCAGGGCTGTTAGT  
CGTGCACAGCGTGCCTGACCTCTGCATGGCGCCAGGGCAAGATGCCGAGGAGATGGTACAATGTGACCGA  
ACTCGGAGGAAGACTGTGCTTCGAGGAGGAGATCCGCCAGATGGTACAATGTGACCGA  
TCCGAGAAGCACGCCCTCCGGTCTCCCTGAGCAGTGCCAACAGCGGAGCTGTACAAGAA  
CAGAGGCTTCTTCACTCTCATTTCTGCCATGCTGCCATGGTCCCAGAGGAGCCTG  
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTCTGCCCTGGAGACCGACAGCATG  
GACCCATTGGGCTGTACCAGGACTGGAGGCCGTGAGGAGTCCCAGCTTGAAGTAAC  
GAGACCATGCCGGGCTCTCAGTGCAGTCCACGTTCTGTTAGCTTAGGAAGAACATCTAGAA  
GTTGTACATATTCAAGAGTTTCCATTGGCAGTGCAGTTCTAGCCAATAGACTTGTCTGAT  
CATAAACATTGTAAGCCTGTAGCTGCCAGCTGCCCTGGCCCCATTCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGCTGCACTGTCTAGTTCTGCTGAATACCTCCATCGATGGGAAC  
TCACCTCTTGGAAAAATTCTTATGTCAAGCTGAAATTCTAATTCTCATCACCTC  
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTAATTCAAGGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAATTCACTCAACCCATGTGGAAATTGATCTATCTACTTCCAGGG  
ACCATTGCCCTCCAAATCCCTCCAGGCCAGAACCTGACTGGAGCAGGCATGGCCCACCCAG  
GCTTCAGGAGTAGGGGAAGCCTGGAGGCCACTCCAGGCCCTGGGACAACCTGAGAATTCCCC  
CTGAGGCCAGTTCTGTCATGGATGCTGCTGAGAATAACCTGCTGCTCCGGTGTACCTGC  
TTCCATCTCCAGGCCACAGCCCTGCCCCACCTCACATGCCCTCCCATGGATTGGGGCCT  
CCCAGGCCCCCACCTTATGTCAACCTGCACTTCTGTTCAAAATCAGGAAAAGAAAAGAT  
TTGAAGACCCCAAGTCTGTCAATAACTGCTGTGGAAAGCAGGGGGAAAGACCTAGAAC  
CCTTTCCCCAGCACTTGGTTTCCAACATGATATTATGAGTAATTATTTGATATGTACA  
TCTCTTATTTCTACATTATTATGCCCCAAATTATATTATGTATGTAAGTGAGGTTG  
TTTGATATTAAAATGGAGTTGTTGT

## **FIGURE 22**

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLIEIKAVALRTVAIKGVHVSRYLCMGADGKMQGLLQYSEEDCAFEE  
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMPLPMVPEEPEDLRGHLESD  
MFSSPLETDSDMPFGLVTGLEAVRSPSFEK

**Signal peptide:**

amino acids 1-22

**Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

**N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

## **FIGURE 23**

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTCGACCTCCTCA  
GAGCAGCCGGCTGCCGCCCGGGAAAGATGGCGAGGAGGAGCCACCGCCTCCTGCTG  
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGTTTCTGCCCAAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAAACCCAA  
AGAAGACTGTTCCCTCCAGATTAGAGTGGAAAGAAACTGGTCGGAGTGTCTCCTTGTCTAC  
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG  
GATCAAAATGTGACAAGAAGTGTGATGCCGGAAATATCGTTGTGAAGTTAGTGCCTCATCTG  
AGCAAGGCCAAACCTGGAAGAGGATACTGACTCTGGAAAGTATTAGTGGCTCCAGCAGTT  
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA  
CAAAGAAGGGAAATCCAGCTCTGAATAACACATGGTTAAGGATGGCATCCGTTGCTAGAAA  
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACACAATGAATAACAAAAACTGGAAC  
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCTGTGAAGCCGCAATT  
TGTTGGATATCGCAGGTGTCCCTGGAAACGAATGCAAGTAGATGATCTCACATAAGTGGCA  
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTCCGTTGTGGCCTTGGTGTATGCTAT  
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA  
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCGTAACTCCAGCACTTGGAAAGG  
CCGGGGCGGGCGGATCACGAGGTCAAGGAGTTCTAGACCAGTCTGCCAATATGGAAACCC  
CATCTCTACTAAAATACAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC  
TTGGGAGACAGGAGAATCACTGAACCCGGGAGGCAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAATAAAATAATA  
AATAAAACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

## **FIGURE 24**

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTSSRLE  
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED  
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD GIRLLENPRLGSQST  
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIIAAVVVA  
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKAAGGSRGQEF

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 130-144, 238-258

**N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

**Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

**N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

**Amidation site.**

amino acids 226-230

## **FIGURE 25**

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG  
AAAGAAGAGGAAGATGTTGGCAACATTATTTAACATGCTCCACAGCCGGACCTGGCAT  
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGATTAAATATTTACTTCTAAATAA  
ATGAATTACTCAATCTCTATGACCACCTATACATACTCCACCTCAAAAAGTACATCAATA  
TTATATCATTAGGAAATAGTAACCTCTCTCCAAATATGCATGACATTGGACAATG  
CAATTGTGGACTGGCACTTATTCTAGTGAAGAAAACCTTGTGGTCTATGGCATTCA  
TTGACAAATGCAAGCATCTCCTTATCAATCAGCTCTATTGAACTTACTAGCACTGACTG  
TGGAATCCTTAAGGGCCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT  
CCGAATTCTATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAG  
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTGGTTACACCCAGATCCATTAT  
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACCTTCCCAGCCAGATTGCC  
AGCTAACACACAGATTCTCTCCTACAGACTAACAAATATTGCAAAACATTATCTCAGTCACCAAT  
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAAATTATCTCAGTCACCAAT  
ATTAATGTAACAAAGATGCCTCAGCTCTTCTGTGTACCTAGAGGAAACAAACTACTGA  
ACTGCCTGAAAATGTCGCGAAGTGCACACTACAAGAACTCTATATTAACTCACA  
TGCTTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTTCTCGACTTCATCTC  
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTTCAAATCTAGAGAT  
TCTGATGATGGGAAAATCAAATTATCAGAATCAAAGACATGAACCTTAAGCCTTATCA  
ATCTTCGCGAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCGG  
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCATGT  
TGCTCTTCAAACAGTTGTAATCTCAAATTGGATCTAAATAAAACTCTATTAAAGGAA  
TACGAAGGGGTGATTCTAGCAATATGCTACACTAAAGAGTTGGGATAAATAATATGCC  
GAGCTGATTCCATCGATAGTCTGCTGTGGATAACCTGCCAGATTAAAGAAAATAGAAGC  
TACTAACACCCCTAGATTGTCTTACATTCCCCAATGCATTTCAGACTCCCCAAGCTGG  
AATCACTCATGCTGAAACAGCAATGCTCTAGTGCCTGTACCATGGTACCATGGTCTG  
CCAAACCTCAAGGAAATCAGCATAACAGTAACCCCATCAGGTGTGACTGTGTCATCCGTTG  
GATGAACATGAACAAAACCAACATTGATTGAGCCAGATTCACTGTTTGCCTGGACC  
CACCTGAATTCCAAGGTCAAATGTTGGCAAGTGCATTCAAGGACATGATGGAATTG  
CTCCCTTTAGCTCTGAGAGCTTCCTCTAATCTAAATGAGAAGCTGGGAGCTATGT  
TTCCTTCACTGTAGAGCTACTGCAGAACACCACAGCCTGAAATCTACTGGATAACACCTCTG  
GTCAAAACCTCTGCCTAATACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAAACACTA  
GATAAAATGGCTAACTCCCAAAGAAGGGGTTATATACCTGTATAGCAACTAACCTAGT  
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAATG  
GCTCTTGAATATTAAAATAAGAGATATTCAAGGCAATTCACTGTTGGTGTCCCTGGAAAGCA  
AGTTCTAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA  
TGCTGCGCAAAGTGCCTGAATACCATCTGATGTCAAGGTATATACTTACTCATCTGAATC  
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTATCAGAAAAACAGAAAAAAA  
TGTGTAAATGTCACCACCAAAGGTTGCACCCCTGATCAAAAAGAGTATGAAAAGAATAATAC  
CACAACACTTATGGCCTGTCTGGAGGCCTTCTGGGGATTATTGGTGTGATATGTCTTATCA  
GCTGCCTCTCCAGAAATGAACGTGATGGTGGACACAGCTATGTGAGGAATTACTACAG  
AAACCAACCTTGCATTAGGTGAGCTTATCCTCTGTGATAAAATCTCTGGGAAGCAGGAAA  
AGAAAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTAGGTTACCAACAAATATGTCC  
AAAAACCAAGGAAACCTACTCCAAAATGAAC

## **FIGURE 26**

MKDMPRLIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT  
FPARLPANTQILLQTNNAKIEYSTDFPVNLTGDLSQNNLSSVTNINVKKMPQLLSVYLE  
ENKLTELPEKCLSELNLQELYINHNLLSTISPGAFIGLHNLLRLHLNSNRLQMINSKWFDA  
LPNLEILMIGENPIIRIKDMNFKPLINLRSVVIAGINLTEIPDNAVLGLENLESISFYDNRL  
IKVPHVALQKVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPD  
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSYHGTIESLPNLKEISIHSNPIRC  
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFPSNLNV  
EAGSYVSFHCRTAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC  
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSKASSKILKSSVKWTAFV  
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE  
YEKNNTTLMACLGGILLGIIGVICLISCLSPEMCDGGHSYVRNYLQKPTFALGELYPPLIN  
LWEAGKEKSTSLKVKATVIGLPTNMS

**Signal sequence:**

amino acids 1-22

**Transmembrane domain:**

amino acids 633-650

**N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

**Tyrosine kinase phosphorylation site.**

amino acids 570-579

**N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

**Cell attachment sequence.**

amino acids 277-280

## **FIGURE 27**

CCCCGGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC  
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTATTGCTGACATTCCAGCATGAATCT  
GGTAGACCTGTGGTTAACCGTTCCCTCTCCATGTGTCTCCTACAAAGTTGTTCTTA  
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCAAGGGCTGTCTTGTCTCCTCTGGG  
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG  
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCATT  
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG  
TGTGCACAAAATGCCTCAATAACCTGAAGGCCAGGCCAGAATTGCCAACAAACCCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC  
AACGTGATCTGTAAAACGTCCGTGGATGAACATGCTGGCAGACCATTCCCTCAATGCTGC  
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTGGCTGGTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAATCAGGAG  
GATGCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCAATTGAGAAAGAAAGAAA  
GTAGTTGCGATTGCACTGAGAAATAAGTGGTTACTTCTCCCATCGTAAACAAACACTACAACA  
ACTTTGTATTCAGTTTTTGAAATTATGCCACTGCTGAACCTTAAACAAACACTACAACA  
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT  
AAGCTACTATCTGAACATTAGTTAGATCCCATCTCACTATTAAATAATGAAATTATTTTTT  
AATTAAAAGCAAATAAAAGCTTAACCTGAACCATGGAAAAA

## **FIGURE 28**

MNLVDLWLTRSLSMCLLQSFVLMILCFHSASMCPKGCLSSSGGLNVTCNSANLKEIPRDL  
PPETVLLYLDNSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLSDLSDNR  
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPF  
NAANDADLCNLPPKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK  
ADEPDDISTVV

**Signal sequence:**

amino acids 1-33

**Transmembrane domain:**

amino acids 205-220

**N-glycosylation site.**

amino acids 47-51, 94-98

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 199-203

**Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

**N-myristoylation site.**

amino acids 37-43, 45-51, 110-116

## **FIGURE 29**

## **FIGURE 30**

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPCECSAQDRAVLCHRKCF  
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTL  
GLRSNRLKLIPLGVFTGLSNLTQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA  
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH  
WPYLDLTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMIHEL  
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSVGNLETLILDSNPLA  
CDCRLLWVFRWRRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVFPDGTLLEVRYAQVQDNGTYL  
CIAANAGGNDNSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI  
IATTMGFISFLGVVLFCVLVLLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 556-578

**N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

**Tyrosine kinase phosphorylation site.**

amino acids 590-598

**N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

## **FIGURE 31**

CCCCACCGCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTCGGTCAAC  
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGGCCAGCC  
AGGGAGCCGGCCGGGAAGCGCGATGGGGCCCCAGCCGCTCGCTCCTGCTCCTGC  
TGTTCGCCTGCTGGCGCCGGCGGGCAACCTCTCCAGGACGACAGCCAGCCCTGG  
ACATCTGATGAAAACAGTGGTGGCTGGTGGCACCGTGGCTCAAGTGCCAAGTGAAGATCA  
CGAGGACTCATCCCTGCAATGGCTAACCTGCTCAGCAGACTCTACTTTGGGAGAAGA  
GAGCCCTCGAGATAATCGAATTCAAGCTGGTTACCTCTACGCCAACGAGCTCAGCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTCACTATGCCGT  
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCACTGGTT  
ATAAAATCTTCATTACGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTTCTGGGAGCAAG  
CCTGCAGCCGGCTCACCTGGAGAAAGGGTACCAAGAACCTCACGGAGAACCAACCGCAT  
ACAGGAAGATCCAATGGTAAAACCTTCACTGTACAGCTCGGTGACATTCCAGGTTACCC  
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC  
AGATCCACCTCTAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCCTCGTGAGGGCCAGAACGCTGTTGCTACACTGTGAGGGTCGCCAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGCCAGGAGAGT  
GCCCTGATCTCCCTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACGCCACCAG  
CAACATGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGCCAGTCCGGTCCCT  
CCTCCCTCAGCACCTACCACGCCATCATCGTGGATCGTGGCTTCATTGTCTTCTGCTG  
CTCATCATGCTCATCTCCTGCCACTACTGATCCGGCACAAAGGAACCTACCTGACACA  
TGAGGCCAAAGGCTCCGACGATGCTCCAGACGCCAGGCCATCATCAATGAGAGCG  
GGCAGTCAGGAGGGACGACAAGAAGGAATATTCATTAGAGGCGCTGCCACTTCCTGC  
GCCCTCCAGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAAC  
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCACCCACCCCTGTACAGAAC  
TTGGGTGCGGTTTGACTCGGTTGGAATGGGAGGGAGGGAGGGAGGGAGGGAGGG  
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAACAATCC  
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGGCCCTGGGTGAGAAAAGCAAAAAACA  
AACAAAAAACAA

## **FIGURE 32**

MGAPAASLLLLLFFACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLKCQVKDHEDSSLQW  
SNPAQQTLYFGEKRALRDNRQLVTSTPHELSIISNVALADEGEYTCSIFTMPVRTAKSLV  
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGQELHGEPTRIQEDPNGK  
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA  
YYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

**Signal sequence:**

amino acids 1-20

**Transmembrane domain:**

amino acids 331-352

**N-glycosylation site.**

amino acids 25-29, 290-294

**Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

**N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 33**

GGGGGTTAGGGAGGAATCCACCCCCACCCCCCAAAACCCCTTCTCTCCTTCTGG  
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCGTGGCGAGCAGGATGGTCGTG  
TTACTTTGTGATGAGATCGGGATGAATTGCTCGCTTAAAAATGCTGCTTGGATTCTGTT  
GCTGGAGACGTCTTTGTTGCGCTGGAAACGTTACAGGGACGTTGCAAAGAGAAGA  
TCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA  
AGTCTGCAGCAGCTTCACTGCCCGACTTCCAGTTTACCATTTCTGCATGGCAATT  
CCTCACTCGACTTTCCCTAATGAGTCGCTAACCTTATAATGCGGTTAGTTGCACATGG  
AAAACAATGGCTTGCATGAAATCGTCCGGGGCTTTCTGGGCTGCAGCTGGTAAAAGG  
CTGCACATCAACAACAAGATCAAGTCTTTCGAAAGCAGACTTTCTGGGCTGGACGA  
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACCCGGGGCTTCCAGG  
ACTTGAACAAGCTGGAGGTGCTCATTTAAATGACAATCTCATCAGCACCCACCTGCCAAC  
GTGTTCCAGTATGTGCCATCACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCC  
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCC  
GGGACTGCACCTGTGATCTGCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC  
CTGATCGGGCGAGTGGTCTGCGAAGCCCCCACAGACTGCAGGGTAAAGACCTCAATGAAAC  
CACCGAACAGGACTTGTGTCCTTGAAAAACCGAGTGGATTCTAGTCTCCGGCGCCCCCTG  
CCCAAGAAGAGACCTTGCTCCGGACCCCTGCCAACTCCTTCAAGACAAATGGGCAAGAG  
GATCATGCCACACCAGGTCTGCTCCAAACGGAGGTACAAAGATCCAGGCAACTGGCAGAT  
CAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAAC  
GTTTACCCCTGCCCTGGGGCTGCGCTGCGACCACATCCAGGTCGGGTTAAAGATGAAC  
TGCAACAAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCCAAGCTCTAACGTGCAGGA  
GCTTTCCCTACGAGATAACAAGATCCACAGCATCCGAAAATCGACTTTGTGGATTACAAGA  
ACCTCATTCTGTTGGATCTGGCAACAATAACATCGTACTGTAGAGAACAAACACTTCAAG  
AACCTTTGGACCTCAGGTGGCTACATGGATAGCAATTACCTGGACACGCTGTCCGGGA  
GAAATTCGGGGCTGCAAAACCTAGAGTACCTGAACTGGAGTACAACGCTATCCAGCTCA  
TCCTCCGGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAACACCTG  
CTGAGGTCCTGCCTGTTGGACGTGTTGCGTGGGTCTCGCTCTCTAAACTCAGCCTGCACAA  
CAATTACTCATGTAACCTCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA  
TAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCCTTCAAGCAGTGGCA  
GAACGCTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTT  
TAGAAAGGATTTCATGCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT  
CGCCACGTTAACTCGCACAGTAAAACAGCAGCTGGGTGGCGAGACGGGACGCACTCC  
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTGGTGTGGTCCGGACTGCTGCTGGT  
GTTTGTACCTCCGCCCTCACCGTGGTGGCATGCTCGTTATCCTGAGGAACCGAAAGC  
GGTCCAAGAGAGACGAGATGCCAACTCCTCCGCGTCCGAGGATTAATTCCCTACAGACAGTCTG  
GACTCTCTACTGGCACAATGGGCTTACAACCGAGATGGGCCCCACAGAGTGTATGACTG  
TGGCTCTACTCGCTCTCAGACTAAAGACCCCAACCCCAATAGGGAGGGCAGAGGGAAAGGCG  
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCCAAATCCCCGCG  
CCATCAGCCTGGATGGCATAAGTAGATAAAACTGTGAGCTCGCACAACCGAAAGGGCCT  
GACCCCTACTTAGCTCCCTCTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA  
GCCAGCTCGCTTTGCTGAGAGGCCCTTTGACAGAAAGCCAGCACGACCCCTGCTGGAAG  
AACTGACAGTGCCCTCGCCCTCGGCCCCGGGGCTGTGGGTTGGATGCCCGGTTCTATAC  
ATATATACATATCCACATCTATATAGAGAGATAGATATCTATTTCCTGTGGATTAG  
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT  
TGTAAATAAGTAACCTTGACTCTGAC

## **FIGURE 34**

MLLWILLLETSLCFAAGNVTGVCCKEKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH  
LFLHGNSLTRLFPNEFANFYNAVSLHMEENGLHEIVPGAFGLQLVKRLHINNNKIKSFRQ  
TFLGLDDLEYLQADFNLLRIDPGAFQDLNKEVLILNDNLISTL PANVFQYVPITHLDLRG  
NRLKTL PYEEVLEQI PGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ  
GKDLNETTEQDLCPLKNRVDSSL PAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGT  
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGCSCDHIPGSGLKMNCNNRNVSSLADLK  
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNY  
LDTLSREKFAGLQNLEYLNVEYNQIQLILPGTFNAMPKLRILILNNNNLLRSLPVDVFAGVSL  
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPKQWAERLGSEVLMSDLKC  
ETPVNFFRKDFMLLSND EICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL  
VPGLLL VFTSAFTVVGMLVFILENRKRSKRRDANS SASEINSLQTVCDSSYWHNGPYNADG  
AHRVYDCGSHSLSD

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 618-638

**N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

**Casein kinase II phosphorylation site.**

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697

**N-myristoylation site.**

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

## **FIGURE 35**

AGTCGACTCGGTCCCCGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC  
TGCACCGGGCCTGGCAGCGCTCCGACACATTCTGTGCGGCCCTAAGGGAAACTGTTGGC  
CGCTGGGCCCGGGGGGATTCTTGGCAGTTGGGGGTCCGTGGAGCGAGGGCGGAGGGG  
AAGGGAGGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC  
AGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTGGAGCAGCTGCGTGCCTGGGGCCTCAG  
AGAATGAGGCCGGCGTTGCCCTGTGCCCTCGAGCGCTCTGGCAGGCCCTGGCCGGCGG  
CGGCGAACACCCCAC TGCCGACCGTGCTGGCTCGGCCTCGGGGCTGCTACAGCCTGC  
ACCA CGCTACCATGAAGCGGCAGCGGCCGAGGAGGAGCCTGCATCCTGCGAGGTGGGGCGCTC  
AGCACCGTGCCTGCGGGCGCCAGCTGCGCCTGTGCTCGCCTCTGCGGGCAGGCCAGG  
GCCGGAGGGGCTCCAAGAACCTGCTGTTCTGGTGCAGTGGAGCGCAGGCCTCCACT  
GCACCCCTGGAGAACGAGCCTTGCGGGGTTCTCTGGCTGTCCTCCGACCCGGCGGTCTC  
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGGGAGATGCGC  
GGTACTCCAGGCCACCGGTGGGGTCGAGCCCGAGGCTGGAAGGAGATGCGATGCCACCTGC  
GCGCCAACGGCTACCTGTCAAGTACCAAGTTGAGGTCTGTGTCCTGCGCCGCCCCGG  
GCCGCTCTAACCTGAGCTATCGCGGCCCTCAGCTGCACAGCGCCGCTCTGGACTTCAG  
TCCACCTGGGACCGAGGTGAGTGCCTGCGCTGGGACAGCTCCGATCTCAGTTACTGCA  
TCGCGGACGAAATCGCGCTCGCTGGACAAACTCTCGGGCGATGTGTTGTGTCCTGCCCC  
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAAC TGCGCTAGACGACTGGGAGG  
CTTTCGCTGCGAATGTGCTACGGGCTTCGAGCTGGGAAGGACGGCCGCTTGTGACCA  
GTGGGGAGGACAGCCGACCCCTGGGGGACCGGGTGCCTGCCCCACCAAGCGCCGGCCACT  
GCAACCAGCCCCGTGCCGAGAGAACATGGCCAATCAGGGTCGACGAGAACGACTGGGAGAGAC  
ACCACTGTCCTGAACAAGACAATTCACTAACATCTATTCTGAGATTCTCGATGGGAT  
CACAGAGCACGATGTCTACCCCTCAAATGTCCTCAAGCCAGTCAAAGGCCACTATCACC  
CCATCAGGGAGCGTGATTTCAAGTTAATTCTACGACTCCTCTGCCACTCCTCAGGCTTT  
CGACTCCTCTCTGCCGTGGCTTCATATTGTGAGCACAGCAGTAGTAGTGTGTTGGGATCT  
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTACGAAAGCCCTCTCCAGCCA  
AGGAAGGAGTCTATGGGCCGCCGGCCTGGAGAGTGATCCTGAGCCGCTGCTTGGGCTC  
CAGTTCTGCACATTGCACAAACAATGGGTGAAAGTCGGGACTGTGATCTGCGGGACAGAG  
CAGAGGGTGCCTGCTGGCGAGTCCCTCTGGCTCTAGTGATGCATAGGAAACAGGGAA  
CATGGGCACCTCTGTGAACAGTTTCACTTTGATGAAACAGGGAAACCAAGAGGAACCTAC  
TTGTGTAATGACAATTCTGCAGAAATCCCCCTCCTCTAAATTCCCTTACTCCACTGAG  
GAGCTAAATCAGAACACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA  
TGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATTTCTATGTTATTGGAGAA  
TTTGGAGAAGTGATTGAACTTTCAAGACATTGAAACAAATAGAACACAATATAATTACA  
TTAAAAAAATAATTCTACCAAAATGAAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT  
ATTGGTTGAAATCCAGGGAAAAAAATAAAAATTAAGGATTGTTGAT

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## **FIGURE 36**

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSIHATMKRQAAEACILRGGALS  
TVRAGAELRAVLALLRAGPGPGGGSKDILFWVALERRSHCTLENEPLRGFSWLSSDPGGL  
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFVLCPAPRPG  
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCG  
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA  
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILMTVLGLVKLCFHESPSSQPR  
KESMGPPGLESDPPEPAALGSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 189-193, 381-385

**Glycosaminoglycan attachment site.**

amino acids 289-293

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

**Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

**N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

## **FIGURE 37**

CGGACCGCGTGGGATTCAAGCAGTGGCTGTGGCTGCCAGAGCAGCTCCCTCAGGGAAACTAAG  
CGTCGAGTCAGACGGCACCATAATCGCCTTAAAAGTGCCTCCGCCCTGCCGGCGCGTATC  
CCCCGGCTACCTGGGCCCGCCCGCGCGGTGCGCGTGAAGAGGGAGCGCGGGCAGCGA  
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAAGCGCCGGTGTGAAGCGCCGGTGGGTGCGGA  
GGGGCGTGTGAGCCGGCGCGCGCGCCGGTGTGCAAACCCCGAGCGTCTACGCTGCCATGA  
GGGGCGCGAACGCCTGGCGCCACTCTGCCTGCTGGCTGCCGCCACCCAGCTCTCGCG  
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT  
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCAAATAGCAAATGTACTTGGAAAATCA  
CAGTTCCCGAAGGAAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTGACAAC  
CTGTGCCGCTATGACTTGTGGATGTGTACAATGCCATGCCAATGCCAGCGCATTGGCG  
CTTCTGTGGCATTTCGGCCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA  
TGATTTCTGATGCCAACACAGCTGGCAATGGCTCATGCCATGTTCTCCGCTGCTGAACCA  
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTTTAAAAC  
CCCCAACTGGCCAGACCGGGATTACCCCTGCAGGAGTCACTTGTGTGGCACATTGTAGCCC  
CAAAGAATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC  
CGATATGATTATGTGGCTGTGTTAATGGCGGGAAAGTCAACGATGCTAGAAGAATTGGAAA  
GTATTGTGGTGTAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTTATTCACT  
TTTATCAGACTTAAGTTAACGCAGATGGTTTATTGGTCACTACATATTCAAGGCCAAA  
AAACTGCCTACAACACTACAGAACAGCCTGTCACCACCATCCCTGTAACCACGGGTTAAA  
ACCCACCGTGGCCTTGTGTCACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT  
GTTCAAGTGAACCTTGTATTAGCCGGCACTGTTATCACAAACCATACTCGCGATGGGAGTTG  
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTGGCGATTCAAGCAGGCC  
CAAGAACATGAGTGCCAGGCTGACTGTCGCTGCAAGCAGTGCCCTCTCAGAACAGGTC  
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGCGAGGAAAATCATGCCAACAGC  
TTTATCATGATGTTCAAGACCAAGAACATCAGAACGCTCTGGATGCCCTAAAAAATAAGCAATG  
TTAACAGTGAACGTGTCCATTAAAGCTGTATTCTGCCATTGCCCTTGAAAGATCTATGTT  
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG  
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCCTCGAGATAGCTGAGGGAAAGTTCTT  
TGCCCTGCTGTCAGAGGGAGCAGCTATCTGATTGGAAACCTGCCACTTAGTGCCTGATAGGA  
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAAGCGTTATTACATCTCTGAAAGGAT  
ATTAGAATTGAGTTGTGTGAAGATGTCAAAAAAAAGATTTAGAAGTGCATATTATAGT  
GTTATTGTTTACCTTCAAGCCTTGCCTGAGGTGTACAATCTTGTCTCGCTTCTA  
AATCAATGCTTAATAAAATTTAAAGGAAAAAA

## **FIGURE 38**

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK  
ITVPEGKVVVLNFRFIDLESDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDYPAVGTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYAVFNGEVNDARRIGKYCGDSPPAPIVSERNELLI  
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN  
YCSSDFVLAGTVITTRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR  
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

**Signal sequence:**

amino acids 1-23

**N-glycosylation site.**

amino acids 355-359

**Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

**Tyrosine kinase phosphorylation site.**

amino acids 199-208

**N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

**Cell attachment sequence.**

amino acids 149-152

## **FIGURE 39**

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCCGGGCTGGGGCGGTGCGCTTCCT  
CCTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCCGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTCAACCTCCCAGGACCTATCTGG  
CTCCAGCCCTCTCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTACACCTG  
CCGGGGACTGGTTGACAGCTTAACAAGGGCTGGAGAGAACCATCCGGGACAACTTGGAG  
GTGGAAACACTGCCTGGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTG  
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTTCGAGTGCACCGCCTGCTGGAGCT  
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC  
CTTCCCTGTCTGGGAAACAGAGAGGCCCTGGCTACGGCAGTGTGAAGGAGAAGG  
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGCTACGGGGTGAAGGCTGTGGCC  
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT  
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGGCAATGCAAGAAGGG  
CTGGGCCCTGCATCACCTCAAGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCA  
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG  
GCCTGCCTAGGCTGCATGGGGCAGGCCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCA  
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGGAGAGA  
ACAAGCAGTGTGAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG  
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGCAGCAGATGTTCTTGGCATCATCTGTGCACTGGCCA  
CGCTGGCTGCTAAGGGCAGTTGGTGTTCACGCCATCTCATTGGGCTGTGGCGGCCATG  
ACTGGCTACTGGTTGTCAGAGCGCAGTGACCGTGTGGAGGGCTTCATCAAGGGCAGA  
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCGAGAGCTTGGCTGCC  
TCCTGCTGGACACTCAGGACAGCTTGGTTATTTTGAGAGTGGGTAAGCACCCCTACCTG  
CCTTACAGAGCAGCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAGGAAAAAGTAGC  
CCTGAAGGTGGATACCATGAGCTCTCACCTGGCGGGACTGGCAGGCTTCACAATGTGTGA  
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG  
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCTGCCAGTTCTGT  
TCTGTGTTACCAACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAAGA  
AAGGTCTTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 40**

MAPWPPKGLVPAVLWGLSLFLNLPGPIWLQSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER  
TIRDNFGGGNTAWEEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLESELVESWWFHKQ  
QEAPDLFQWLCSDSLKLCGPAGTFGPSCLPGTERPCGGYQCEGEGRGGSGHCDCQAG  
YGGEACGQCGGLGYFEAERNASHLVCACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE  
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE  
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG  
IIICALATLAAGDVLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

**Signal sequence:**

amino acids 1-29

**Transmembrane domain:**

amino acids 372-395

**N-glycosylation site.**

amino acids 79-83, 205-209

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

**Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

**N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

**Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

**EGF-like domain cysteine pattern signature.**

amino acids 181-193

## **FIGURE 41**

TGAGACCCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA  
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGACTCTGGGTGTTGCCCTGGCCAGCCCCGGG  
GCCGCCCTGACCGGGGAGCAGCTCCTGGGAGCCTGCGCTGCCAGCTGCAGCTCAAAGAGGT  
GCCCACCCCTGGACAGGGCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT  
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTCAGCCAGAGC  
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGTTCGG  
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTCAGGCCGTGCTGCCGCTTCCAGG  
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGCGGCTGTCCCCGCGCAGGCCCGGGCC  
CGGGTGACCGTCGAGTGGCTGCGCGTCCCGACGGCTCCAACCGCACCTCCCTCATCGA  
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCCTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG  
GAGCATCTGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTGCCTCGCAGGGGGC  
GCCAGCCGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG  
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG  
ATGTACATTGACCTGCAGGGATGAAGTGGCCGAGAACTGGGTGCTGGAGCCCCCGGGCTT  
CCTGGCTTATGAGTGTGTGGCACCTGCCGGCAGCCCCCGAGGCCCTGGCCTTCAAGTGGC  
CGTTTCTGGGGCCTCGACAGTGCATGCCCTCGGAGACTGACTCGCTGCCATGATCGTCAGC  
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA  
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCTGCCAGGAGGCTCCAGCCATAGGCGCCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGTGAGGGTACCAAGGAGAGCTG  
GCGATGACTGAAGTGCCTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT  
CCTCTGACAAGTTACCTCACCTAATTTGCTCTCAGGAATGAGAATCTTGGCCACTGGA  
GAGCCCTGCTCAGTTCTCTATTCTATTCACTGCACTATATTCTAACGCACTTACAT  
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCANTGTGTCATTGTTACTTGTCCGTAC  
TGGATCTGGCTAAAGTCCTCCACCACCTGGACCTAACGACCTGGGTTAAGTGTGGGT  
TGTGCATCCCCAATCCAGATAATAAGACTTTGTAAAACATGAATAAACACATTTATTCT  
AAAA

## **FIGURE 42**

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLRLQLQLKEVPTLDRADMEELVIPHVRQAQYV  
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP  
VPKAALHRHGRLSPRSARARVTVEWLVRDDGSNRTSLIDSRLVSHESGWKAFDVTEAVNF  
WQQLSRPRQPLLLQSVSQREHLGPLASGAHKLVRFASQGAPAGLGEPEQLELHTLDLGDYGAQ  
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPPEALAFKWPF  
LGPRQCIASETDSLPMIVSIKEGGRTTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 158-162

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

**Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

**N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

**Amidation site.**

amino acids 74-78

**TGF-beta family signature.**

amino acids 282-298

## FIGURE 43

GTCTGTTCCCAGGAGTCCTCGGCGGCTGTTGTCAGTGGCCTGATCGCGATGGGGACAAA  
GGCGCAAGTCGAGAGGAAACTGTTGTCCTCTTCATATTGGCGATCCTGTTGCTCCCTGG  
CATTGGGCAGTGTACAGTGCACCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT  
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTCTTCTCCCCGTGTGGAGTGGAAAGTTGACCA  
AGGAGACACCAACCAGACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGG  
TGACCTTCTGCCAACCTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGGCGAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTGCCACCATGGGAACCGGG  
CAGTGCTGACATGCTCAGAACAAAGATGGTCCCCACCTCTGAATAACACACTGGTTCAAAGAT  
GGGATAGTGTGCTACGAATCCAAAAGCACCCGTGCCCTCAGCAACTCTCCTATGTCCT  
GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCTGTCAGCCTCTGATACTGGAGAATACA  
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTCAAATGCTGTGCGCATGGAGCT  
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTGTAACCTGATTCTCCTGGGAAT  
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA  
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTCTGGTGTGAGCCTGGCTCACCCTATCATCTGCATTGCTTACT  
CAGGTGCTACCGGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCTTATTGTCTTC  
TACACCCCACAGGGCCCCCTACTTCTCGGATGTGTTTAATAATGTCAGCTATGTGCC  
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACTGTTAAA  
GTGTTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAGTAGACAGAAAAATGGCGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGC  
TGGCAGGGATCTTGAAATAGGTATCTTGAGCTTGGTCTGGCTCTTCTGTACTGAC  
GACCAGGGCCAGCTGTTCTAGAGCGGGATTAGAGGCTAGAGCGGCTGAAATGGTTGG  
TGATGACACTGGGTCTTCCATCTCTGGGCCACTCTCTGTCTTCCATGGGAAGTG  
CCACTGGATCCCTGCCCTGCTCCTGAATACAAGCTGACTGACATTGACTGTCTGT  
GGAAAATGGGAGCTTGTGGAGAGCATAGTAAATTTCAGAGAACCTGAAGCCAAAAG  
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGCGCAGTGGCTCACGCC  
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGAGTTGGGATCAGCCTGACCA  
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAAAGAGCAAACCTCCAGCTCAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEW  
KFDQGDTTRILVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV  
KLIVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPPSEYTWFKDGI VMPTNPKSTRAFSNS  
SYVLNPTTGEVFDPLSASDTGEYSCEARNGYGT PMTSNAVRMEAVERNVGVIVAAVLVTLI  
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 238-255

**N-glycosylation site.**

amino acids 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

**Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

## **FIGURE 45**

CAGCGCGTGGCGGCCGCTGTGGGACAGCATGAGCGCGGTTGGATGGCGCAGGTTGGA  
GCGTGGCGAACAGGGCTCTGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT  
GGAGGCCGCGAGCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGGCCAGCTCAG  
GCTCGTCCCACCCACCAAGTTCCAGTGCGCACCAGTGGCTTATGCGTGCCCTCACCTGG  
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC  
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA  
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA  
GGCGAGCTCGTTGCACGCTGAGCGATGACTGCATTCACTCACGTGGCGCTGCACGGCCA  
CCCAGACTGTCCGACTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCGGAAG  
GGGATGCCACAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTCACCTCTCAGGAATGCC  
ACAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTCCCCCTGTGCGGAATGCCACATCCTC  
CTCTGCCGGAGACCAGTCTGGAAAGCCCAACTGCCTATGGGTTATTGCAGCTGCTGCGGTGC  
TCAGTGCAAGCCTGGTACCGCCACCCCTCCTCTGGCTGGCTCCGAGCCAGGAGCGC  
CTCCGCCACTGGGTTACTGGTGGCATGAAGGAGTCCCTGCTGTCAGAACAGAAC  
CTCGCTGCCCTGAGGACAAGCACTGCCACCACCGTCACTCAGCCCTGGCGTAGCCGGACA  
GGAGGAGAGCAGTGATGCGGATGGGTACCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT  
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC  
TGGACACTCCCTATGGAGATCCGGGAGCTAGGATGGGAACTGCCACAGCCAGAACCTGAG  
GGGCTGGCCCCAGGCAGCTCCCAGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG  
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

## **FIGURE 46**

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR  
TSGLCVPLTWRCDRDLDSDGSDEEECRIEPCQKGQCPCPCTGVSDCSGGTDKKL  
RNCSRLAACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELCGTNEILPEGDATTMGPPVT  
LESVTSLRNATTMGPPVTLESPVSGNATSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL  
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

**Signal sequence:**

amino acids 1-30

**Transmembrane domain:**

amino acids 230-246

**N-glycosylation site.**

amino acids 126-130, 195-199, 213-217

**Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

**N-myristoylation site.**

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,  
224-230, 230-236, 263-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 44-55

**Leucine zipper pattern.**

amino acids 17-39

## **FIGURE 47**

CCCACCGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCAGCAGAGGTGCGCACAGATGCGG  
GTTAGACTGGCGGGGGAGGAGGCGGAGGAGGAAGGAAGGAAAGCTGCATGCATGAGACCCACAGA  
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG  
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG  
GCCGTGATCCTGTGGTTAGCTGGCGTGTGCTTCGGCCCTGCACAGCTCACGGCGGGTT  
CGATGACCTCAAGTGTGTGCTGACCCGGCATTCCGAGAATGGCTTCAGGACCCCCAGCG  
GAGGGGTTTCTTGAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG  
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCTAGGCTGGATCCAAGTGA  
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA  
ACAAGACATATAGACATGGAGAGAAGCTAACATCACTTGTATGAAGGATTCAAGATCCGG  
TACCCGACCTACACAATATGGTTCAATTATGTCGCGATGATGGAACGTGGAATAATCTGCC  
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTAATGGCTATGTAACATCTGAGC  
TCCAGACCTCCTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT  
GATGGGTCTCGGTATCTTGAGTGCTTACAAAACCTTATCTGGCGTCCAGCCCACCCGGTG  
CCTTGCTCTGGAAGCCAAGTCTGTCCACTACCTCAATGGTAGTCACGGAGATTCGTCT  
GCCACCCGGCCTTGTGAGCGTACAACCACGGAACGTGGTGGAGTTACTGCGATCCT  
GGCTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCCCTTC  
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA  
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGGTGTGCTCGTCATC  
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTTCCCCCAGGGGGCTCCCCGGAG  
TTCCAGCAGTGACCCCTGACTTGTGGTAGACGGCGTCCCCGTATGCTCCGTCTATG  
ACGAAGCTGTGAGTGGCGGTTGAGTGCCTTAGGCCCCGGTACATGGCTCTGTGGGCCAG  
GGCTGCCCTTACCCGTGGACGACCAGAGCCCCCAGCATAACCCGGCTCAGGGACACGGA  
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTGAGCTGCTCCAAA  
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCCCTGCTCGACAAACCTGACATA  
ATTGCCAGCAGGAGGGAGGTGGCATCCACCAGGCCAGGCATCCATGCCCACGGT  
GTTGTTCTAAGAAACTTGATTGATTTCCAAAGTGTCTGAAGTGTCTCTCAA  
ATACATGTTGATCTGTGGAGGTGATTCTTCTCTGGTTAGACAAATGTAACAA  
AGCTCTGATCCTTAAATTGCTATGCTGATAGAGTGGTAGGGCTGGAAGCTTGATCAAGTC  
CTGTTCTTCTTGACACAGACTGATTTAAAGNAAAAAA

## **FIGURE 48**

MYHGMNPSNGDFLEQQQQQQQQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGGVFFEGSVARFHCQDGFKLKKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI  
PQIEDAEIHINKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPIQGGCLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT  
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS  
VSGSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVLFLRN

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 325-344

**N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

**Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

**N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

## **FIGURE 49**

CCCCACCGCGTCCGCTCCCGGCCCTCCCCCCCCGCCCTCCCGTGCCTGGCTCGGTGGCTAGAGA  
TGCTGCTGCCCGGGTTGCAGTTGTCGCGCACGCCCTGCCGCCAGCCGCTCCACCGCCGT  
AGCGCCCGAGTGTGGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGAAACCGCGTACAGG  
CCGTGCTGCCGTGCTGGTGGGGCTGCCGCCAGGGTCCGCTGAGTGCC  
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTGTTA  
TAAAGTCATTTACTTCATGATACTTCTCGAAGACTGAACTTGAGGAAGCCAAGAACGCCT  
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA  
AAGTTCATTGAAAACCTCTGCCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCCGTGA  
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT  
CACAATTAGGAACTGGTATGGATGAGCCGTCTGCCAGCGAGGTCTGCCGTGGTCATG  
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGATGATGA  
CCGGTGCACATGAAGAACAAATTCATTGCAAATATTCTGATGAGAACCCAGCAGTCCT  
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG  
GAAGAAGATGCCAAAAAAACATTAAAGAAAGTAGAGAACGCTGCCCTGAATCTGGCCTACAT  
CCTAATCCCCAGCATTCCCTCTCCTCCTCTGTGGTACCAACAGTTGTATGTTGGTTT  
GGATCTGTAGAAAAAGAACGGGAGCAGCCAGACCCCTAGCACAAAGAACACACCATC  
TGGCCCTCTCCTCACCAAGGGAAACAGCCGGACCTAGAGGTCTACAATGTACAAAGAAAACA  
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTCTATTCCAGTGTGTT  
CGGGAGAACCACTCCGATGACATGTCTGTACTATGACAACATGGCTGTGAACCCATCA  
GAAAGTGGTTGTGACTCTGGTGAGCGTGGAGAGTGGATTGTGACCAATGACATTATGA  
GTTCTCCCCAGACCAAAATGGGAGGAGTAAGGAGTCTGGATGGTGGAAAATGAAATATATG  
GTTATTAGGACATATAAAACTGAAACTGACAACAAATGGAAAAGAAATGATAAGCAAATC  
CTCTTATTTCTATAAGGAAATACACAGAACGGTCTATGAAACAAGCTTAGATCAGGTCTGT  
GGATGAGCATGTGGTCCCCACGACCTCTGTGGACCCCCACGTTGGCTGTATCCTTTAT  
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAACGGTACCTGCCAGGTCTGGCACATAGTA  
GAGTCTCAATAATGTCACTTGGTTGGTTGTATCTAACCTTAAGGGACAGAGCTTACCTG  
GCAGTGATAAAAGATGGCTGTGGAGCTGGAAAACCACCTCTGTTCTGCTATACAG  
CAGCACATATTATCATAAGACAGAACGGAAATCCAGAACATTCTCAAAGCCCACATATGGTAGCAG  
GTTGGCCTGTGCATGGCAATTCTCATATCTGTTTTCAAAGAACAAATCAAATAAGA  
GCAGGAAAAAA

## **FIGURE 50**

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL  
NFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDL  
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY  
SDEKPAVPSREAEGEETELTPVLPEETQEEAKKTFKESREAALNLAYILIPSIPLLLL  
VTTVVVCWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL  
KNISFRVCSCGEATPDDMSCDYDNMAVNPSSEGFTLVSVESGFVTNDIYEFS  
GWVENEIYGY

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 117-121, 312-316

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

**Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

**N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

## **FIGURE 51**

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCGCAGAAGACTTGT  
GTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT  
GTTCAGCATGCGTTGTGGACCCCAGTGGCGTCTGACCTCGCTGGCGTACTGCCTGCACC  
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGGCCAGTGTCCGGTCACCGCAGC  
CTGCTGAAGTTGAAAATGGTGCAGGTGTTGACACGGGGCTGGAGTCCTCTCAAGCC  
GCTCCCCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC  
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT  
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCATT  
GCAGCAAATGTTGCCTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC  
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG  
GAGTCCACCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT  
CCACACTGATGAAGCAGATTAGAAGTCTTGTATCCAACTACCAAAGCTGCTGGAGCCTGA  
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG  
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT  
GGACAACGTGGCTGCCAGCAGGCACACAAACCTCCAAGCTGCCCATGCTGAAGAGATTG  
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCATTCCCTCACATCCTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG  
TGACCTTCATACCGCTCTTAATGACCCCTGGGATTTGACCACAAATGGCCACCGTTGCT  
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA  
TTACCAACGGGAAGGGAGCAGGTGCCAGAGGTTGCCCTGATGGCTCTGCCCTGGACATGT  
TCTTGAATGCCATGTCAGTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACGTATTATAAAAGCAGGATGTGTTGATT  
TTAAAATAAGTGCCTTATACAATG

## **FIGURE 52**

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR  
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL  
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE  
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD  
FFIILLDNVAAEQAHNLPLSCPMLKRFARMIEQRADVTSLYILPKEDRESLQMAVGPFHLIES  
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

**Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

**Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site.**

amino acids 280-288

**N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site.**

amino acids 216-220

**Leucine zipper pattern.**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

## **FIGURE 53**

CTCCTCTAACATACTTGCAGCTAAACTAAATATTGCTGCTGGGGACCTCCTTAGCCT  
TAAATTCAGCTCATCACCTCACCTGCCTTGGTCATGGCTCTGCTATTCTCCTTGATCCTT  
GCCATTGACCAGACCTGGATTCCCTAGCGTCCATCTGGAGTGCCTGGTGGGGCCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGCACCGTGTGATG  
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCGGAGCTGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA  
ATCAGTCAGTTGCACAGAACAGAACAGAACATGGCTCAGTGTGAGCAAGAACAGTTATG  
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTTTCTCCCCA  
GTCCCAGAGGGTGTCAAGGCTGGCTGACGGCCCTGGCATTGCAAGGGACGCGTGGAAAGTGAA  
GCACCAAGAACAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGAAAGGTGG  
TGTGCCGGCAGCTGGATGTGGAGGGCTGTACTGACTCAAAACGCTGCAACAAGCATGCC  
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAACGAAACCTTCA  
GGATTGCCCTCTGGCCTTGGGGAAAGAACACCTGCAACCAGATGAAGAACACGTGGTCG  
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGAACACCTCTGCTCTGGCGACTG  
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTCTGTGATGACAACACTGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGCTGGGAAGTCCCTCTCCCTCAGAGACCGGA  
AATGCTATGCCCTGGGTTGGCCGCATCTGGCTGGATAATGTTGTTGCTCAGGGAGGAG  
CAGTCCCTGGAGCAGTGCACAGACAGATTTGGGTTTCACGACTGCACCCACCAGGAAGA  
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA  
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGATGAACACTGATCT  
TCTTCTGCCCTGGACTGGACTTAACTTGGTGCCTGATTCTCAGGCCTCAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTCTCAGGCCATCAGACATAGTTGGAACATACATCA  
CCACCTTCCTATGTCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTAT  
CAAATCTAAATACATTCTCACACACACACACACACACACACACACACACACACATA  
CACCATTGCTCTGTTCTCTGAAGAACTCTGACAAAATACAGATTTGGTACTGAAAGAGA  
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGAATTGTTATGGGTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTATTACAATAATAAGATAGCAC  
TATGTGTTCAAA

## **FIGURE 54**

MALLFSLILAICTRPGLASPGVRLVGGHLRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC  
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC  
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNWYTVCQGTGWSLRAAKVVCRQLGCGRAVL  
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG  
GDNLCSGRLEVHLKGWGSVCDDNWGEKEDQVVKQLGCGKSLSPSFRDRKCYGPGVGRIDL  
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

**Signal sequence:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

**N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

**Amidation site.**

amino acids 196-200

**Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

## **FIGURE 55**

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACCGCGTCCGGACCGTGGCGGACCGTGGCCGGCTACCAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCTGGG  
CGTCTCGGCCTCTCCGGCTGCTGCAGTGGGTGCGCGGGAAAGGCCTACCTGCGGAATGCTG  
TGGTGGTGATCACAGGCGCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTATGCT  
GCGGGTGCTAAACTGGTGCTCTGTGGCCGAATGGTGGGCCCTAGAAGAGCTCATCAGAGA  
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC  
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC  
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACACCACAGTGG  
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCAGTTGCTCTAACGAAAGCCTCC  
TGCCCTCCATGATCAAGAGGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCCCTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA  
CTGTCTCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA  
TCCACACCAACCTCTGTAAATGCCATCACCAGGATGGATCTAGGTATGGAGTTATGGAC  
ACCACCAAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGTGGG  
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTGGCTGTTATTCGAA  
CTCTGGCTCCTGGCTCTTCAGCCTCATGCCCTCCAGGGCCAGAAAAGAGCGGAAATCC  
**AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGAGAAGCAGCACTTTAGGCTTGC**  
TTACTCTACAAGGGACAGTTGCATTGAGACTTTAATGGAGATTGTCTACAAGTGG  
AAAGACTGAAGAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA  
AGCTTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT  
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAGGGCGGCCGACTCTAG  
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCAACTTGTTATTGCAGCTTATAATGGTTAC

## **FIGURE 56**

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKEAKVFYAAGA  
KLVLCGRNNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL  
VNNAGISYRGTIMDTTVDVKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI  
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT  
AQGRSPVEVAQDVLAAGKKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 104-120, 278-292

**N-glycosylation site.**

amino acids 228-232

**Glycosaminoglycan attachment site.**

amino acids 47-51

**Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

**Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

**N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

**Amidation site.**

amino acids 265-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17

## **FIGURE 57**

CCCCACCGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTAGAGTGGTAAAAAA  
AAAAAAAAACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTCTCTGGACATCCTC  
CTGCTTCTCCGTTACTGATCGCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCTAA  
GAGGAGAAAATCAGTCACCGCGAAATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA  
GACTGACTGCCTATGAATTGCTAAACTAAAAGCAAGCTGGTCTCTGGATATAAATAAG  
CATGGACTGGAGGAAACAGCTGCCAATGCAAGGGACTGGTGCCAAGGTTCATACCTTGT  
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG  
GAGATGTTAGTATTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTGTTGCTACA  
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGCACATTCTGGACTACAAA  
GGCATTCTTCTGCAATGACGAAGAATAACCATGCCATTGTCACTGGCTTCGGCAG  
CTGGACATGTCTCGTCCCCTTACTGGCTTACTGTTCAAGCAAGTTGCTGCTGTTGGA  
TTTCATAAAACTTGACAGATGAACTGGCTGCCTACAAATACTGGAGTCAAAACAAACATG  
TCTGTGTCCTAATTCGTAACACTGGCTTCATCAAAATCCAAGTACAAGTTGGACCCA  
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG  
ATTTTATTCCATCTCTATAGCTTTTAACAACATTGAAAGGATCCTTCCTGAGCGTTT  
CCTGGCAGTTAAAACGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA  
AAGCGCAATAAGCACCTAGTTCTGAAAATGATTACCAAGGTTAGGTTGATGTCATCTA  
ATAGGCCAGAATTTAATGTTGAACCTCTGTTTTCTAATTATCCCCATTCTCAATA  
TCATTTGAGGCTTGGCAGTCTCATTACTACCACTTGTCTTAGCCAAAAGCTGATT  
ACATATGATATAAACAGAGAAATACCTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA  
CCAAAATGACTTATTAAAATAATTCCAAGATTATTGTGGCTCACCTGAAGGCTTGCAA  
AATTGTACCATAACCGTTTATTAAACATATATTATTGATTGACTTAAATTGTTG  
ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAAACTCAAGCTCTCTAAATAAAA  
TGAAGGACTATATCTAGGGTATTCACAATGAATATCATGAACCTCAATGGTAGGTTTC  
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACTCACATTCCAATGCCAAACATTCT  
GCACAGGGAAAGCTAGAGGTGGATACACGTGTGCAAGTATAAAAGCATCACTGGGATTAAAG  
GAGAATTGAGAGAAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA  
AA  
AA

## **FIGURE 58**

MKFLLDILLPLLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV  
YTSDFLFTQDPQIEKTFEVNVLAHFWTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

**Signal sequence:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34, 283-287

**Casein kinase II phosphorylation site.**

amino acids 52-56, 95-99, 198-202, 267-271

**N-myristoylation site.**

amino acids 43-49, 72-78, 122-128, 210-216

## **FIGURE 59**

CCACCGCGTCCGGACCGCGTGGTCGACTAGTTAGATCGCGAGCGGCCGCCGGCTC  
AGGGAGGAGCACCGACTCGGCCGCACCTGAGAGATGGTGGTGCATGTGGAAGGTGATTG  
TTTCGCTGGCTGTGATGCTGGCCCTGTGATGGCTGTTCGCTCCCTATAACAGAACT  
GTTCCATGCCACCTAAGGGAGACTCAGGACAGCATTATTCACCCCTACATTGAAGC  
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGTCGGCCCTTCCAGGACTGAACATGA  
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTCTGGTTC  
TTCCCAGCTCAGATAAGCCAGAAGATGCCAGTAGTTCTCTGGCTACAGGGTGGCCGG  
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGCCTTATGTTGTCACAAGTAACATGA  
CCTTGCCTGACAGAGACTTCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA  
GTGGGCACAGGCTTCAGTTACTGATGATAACCAACGGATATGCAATGAGGACGATGT  
AGCACGGGATTATACAGTGCACTAATTCAAGTTTCCAGATATTCTGAATATAAAAATA  
ATGACTTTATGTCACTGGGAGTCTTATGCAAGGAAATATGTCAGCCATTGCACACCTC  
ATCCATTCCCTCAACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA  
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGAGAATTCTGTACCAAATTGGCT  
TGTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCATGAATGCATAGAACACATC  
AGGAAGCAGAACTGGTTGAGGCCTTGAAGAAATACTGGATAAAACTACTAGATGGCAGCTAAC  
AAGTGATCCTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTGCCTG  
GCACGGAACCTGAGGATCAGCTTACTATGAAATTGGTCACTCCCAGAGGTGAGACAA  
GCCATCCACGTGGGAATCAGACTTTAATGATGGAACATAGTTGAAAGTACTTGCAGA  
AGATACAGTACAGTCAGTTAACCCATGGTAACTGAAATCATGAATAATTAAAGGTTCTGA  
TCTACAATGCCAACGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTGATGGC  
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTGAAAGATCTTAA  
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCAGGGTGAATTCCATCAGGTAAATTATC  
GAGGTGGAGGACATATTACCTTACGACAGCCTCTGAGAGCTTGACATGATTAATCGA  
TTCATTATGGAAAAGGATGGATCCTTATGTTGAAAACTACCTCCAAAAGAGAACAT  
CAGAGGTTTCATTGCTGAAAAGAAATCGTAAAACAGAAAATGTCATAGGAATAAAAAAA  
TTATCTTTCATATCTGCAAGATTTCATCAATAAAAATTATCCTGAAACAAGTGAGC  
TTTGTGTTGGGGGAGATGTTACTACAAAATTACATGAGTACATGAGTAAGAATTACA  
TTATTTAACTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAAGATGTATAATGA  
AATTTAGGGTCTTGAATAGGAAGTTAATTCTTAAGAGTAAGTGAAGAAGTGCAGTTG  
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT  
GTTGGAAATATTATGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA  
TAGTTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAACATTCTTGAAATA  
AAAATATTATATAAAAGTAAAAAA

## **FIGURE 60**

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDSGQPLFLTPYIEAGKIQKGREL  
SLVGPFPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPyVVTTSNMTLRDRDFPWTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF  
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGIAIGDGYSDPESIIGG  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLGDLTSDPSYFQNV  
TCNSYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGQTFNDGTIVEKYLREDTVQSVKPWL  
TEIMNNYKVLINYNGQLDIIIVAAALTERSLMGMDWKGSQEYKKAEKVVWKIFKSDSEVAGYIRQ  
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

**Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

**Tyrosine kinase phosphorylation site.**

amino acids 423-432

**N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

**Serine carboxypeptidases, serine active site.**

amino acids 200-208

**Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

## **FIGURE 61**

CGAGGGCTTCGGCTCCGAATGGCACATGTGGGAATCCCAGTCTTGTGGCTACAACAT  
TTTCCCTTCCTAACAAAGTCTAACAGCTGTTAACAGCTAGTGATCAGGGGTTCTTCTT  
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTT  
CCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG  
TCTAAAATAGGAAGGAATTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC  
CTGGGGGAGGGCCTGCCTAACAAAGCTTCAAAAACAGGAGCGACTTCACTGGCTGGGAT  
AAGACGTGCCGGTAGGATAGGAAAGACTGGGTTAGTCTTAATATCAAATTGACTGGCTGGG  
TGAACCTAACAGCCTTTAACCTCTGGGAGATGAAAACGATGGCTTAAGGGCCAGAAA  
TAGAGATGCTTGTAAAATAAATTTAAAAAAGCAAGTATTTATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAGGATTCCCTAACATTCCTAACAGGGAGAAAGTATGTTAAAATA  
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAACCAAGGATGGGACCTGGTCT  
AGGCCAGCCTCTTGCTCCTCCGGAAATTATTGGTCTGACCCTCTGCCTTGTGTTT  
GCAGAATCATGTGAGGGCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT  
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCTGGAGGTGG  
ACAGCCGCTCTGTGGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCAGCAGCCGGC  
ATGCCTCAGTTAGCACCTTCACTCTGAGAATCGTACTGGACCTCAACCACCTGACCGT  
CCACCAAGGGACGGGGCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA  
ACCTGACCATCCAGGTGGCTCATAGAACAGGGCAGAAGAGGACAACAAGTCTGTTACCCG  
CCCCTCATCGTGCAGCCCTGCAGCGAAGTGCTACCCCTACCAACAATGTCAACAAGCTGCT  
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGAGCCTCTACCAGGGGTCTGCA  
AGCTGCTGCGGCTGGATGACCTTTCATCTGGTGGAGCCATCCACAAGAAGGAGCACTAC  
CTGTCCAGTGTCAACAAGACGGGACCATGTACGGGTGATTGTGCGCTTGAGGGTGAGGA  
TGGCAAGCTCTTCATGGCACGGCTGTGGATGGAAGCAGGATTACTTCCGACCTGTCCA  
GCCGGAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT  
TTTGTCTCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCCACTTGACAT  
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCGAGA  
CCCCTGAGGGTGTGCCATCAACTCCGCTGGAGACCTCTACACCTCACGCATCGTGC  
CTCTGCAAGGATGACCCCAAGTCCACTCATACGTGTCCTGCCCTGGCTGCACCCGGC  
CGGGGTGGAATACGCCCTCCTGCAGGCTGCTACCTGGCCAAGCCTGGGACTCACTGGCCC  
AGGCCTTCAATATCACCAGCCAGGACGATGTACTCTTGCCATCTTCTCAAAGGGCAGAAG  
CAGTATCACCACCCGCCGATGACTCTGCCCTGTGTGCCCTCCCTACCGGGCATCAACTT  
GCAGATCAAGGAGGCCCTGCAGTCCTGCTACCAAGGGCGAGGGCAACCTGGAGCTCAACTGGC  
TGCTGGGAAGGACGTCCAGTCACGAAGGCCCTGTCCCCATCGATGATAACTTCTGTGGA  
CTGGACATCAACCAGCCCTGGGAGGCTCACTCCAGTGGAGGGCTGACCTGTACACCAC  
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTACAACGGCTACAGCGTGGTTTG  
TGGGGACTAAGAGTGGCAAGCTGAAAAGGTAAAGAGTCTATGAGTTAGATGCTCAAATGCC  
ATTCACCTCCTCAGCAAAGAGTCCCTTGGAGGTAGCTATTGGTGGAGATTAACTATAG  
GCAACTTATTTCTGGGAACAAAGGTGAAATGGGGAGGTAAGAAGGGTTAATTTGTG  
ACTTAGCTCTAGCTACTCCTCCAGGCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA  
TTCAATATTCCTAAACTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAAA

## **FIGURE 62**

MGTLGQASLFAPPNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLTAAPLSMEQRQPWP  
RALEVDRSVVLLSVVVLLAPPAAGMPQFSTFHSENRDWTFNHLTGHQGTGAVYVGAINRV  
YKLTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTNNVNKLIIIDYSENRLLACGSL  
YQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY  
FPTLSSRKLPARDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL  
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHYSVSLPFGCTRAGVEYRLLQAAYLAKP  
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSAFCPIRAINLQIKERLQSCYQGEQN  
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG  
YSVVFVGTSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

**Signal sequence:**

amino acids 1-32

**Transmembrane domain:**

amino acids 71-87

**N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

**Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

## **FIGURE 63**

AGGCTCCGCGCGGGCTAGTGCAGACTGGAGTGGGAAACCCGGGTCCCCCGCGCTTAGAGAACACGCG**GATGACCA**  
CGTGGAGCCTCCGGCGAGGCCGGCCGCACGCTGGGACTCCTGCTGCTGGTCTTGGCTTCCCTGGCTCC  
GCAGGCTGGACTGGAGCACCCCTGGTCCCTCTGGGCTCCGCATCGACAGCTGGGCTGCAGGCCAAGGGCTGA  
ACTTCATGCTGGAGGATTCCACCTCTGGATCTTCGGGGCTCCATCCACTATTCCGTGTGCCAGGGAGTACT  
GGAGGGACCGCCTGCTGAAGATGAAGGCTGTGGCTGAACACCCCTCACACCTATGTCAGGTTGGAACTGCATG  
AGCCAGAAAGAGGCAAATTGACTTCCTGGAACCTGGACCTGGAGGCCCTCGCTGATGGCCGCAGAGATCG  
GGCTGTGGGTGATTCTGCGTCCAGGCCCTACATCTGAGATGGACCTCGGGGCTTGCCCAGCTGGCTAC  
TCCAAGACCCCTGGCATGAGGCTGAGGACAACCTACAAGGCTCACCGAAGCAGTGGACCTTATTGACCACC  
TGATGTCCAGGGTGGTGCACACTCCAGTACAAGCGTGGGGACCTATCATTGCCGTGCAGGTTGGAGAATGAATATG  
GTTCTATAATAAGACCCCGCATACTGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTGGAACTGC  
TCCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTGTCAGGGAGTCTTGGCCACCATCAACTTGCAGT  
CAACACACGAGCTGCAGCTACTGACCACCTTCTTCAACGTCCAGGGGACTCAGGCCAAGGATGGTGTGGAGT  
ACTGGAGGGGGGGTGGTGAACGACTCGTGGGGAGGCCCTCACACCTATCTGGATTCTTGTGGAGTTTGAAAACCGTGT  
CTGCCATTGTGGACGCCGGCTCCATCAACCTCTACATGTTCCACGGAGGCCAACATTGGCTTCAATGAATG  
GAGCCATGCACTTCATGACTACAAGTCAGATGTCACAGCTATGACTATGATGCTGTGTCAGAGAACGGCG  
ATTACACGGCCAAGTACATGAAGCTCGAGACTTCTCGGCTCCATCTCAGGATCCCTCTCCCTCCCCCACCTG  
ACCTTCTTCCAAGATGCCGTATGAGCCCTTAACGCCAGCTTGTAACCTGTCTGTGGGACGCCCTCAAGTACC  
TGGGGGAGCCAATCAAGTCTGAAAAGCCCATAACATGGAGAACCTGCCAGTCATGGGAAATGGACAGTCCT  
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCACGTGCATGATGGGGCAGG  
TGTGTTGTGAAACACAGTATCCATAGGATTCTTGACTACAAGACAACGAAGAGATTGCTGTCCCCCTGATCCAGGGTT  
ACACCGTGTGAGGATCTGGTGGAGAATGTGGCGAGTCAACTATGGGAGAATATTGATGACCAGCGCAAAG  
GCTTAATTGGAAATCTCTATCTGAATGATTCAACCTGAAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA  
GCTTCTTCAGAGGTTGGCCTGGACAAATGGNTTCCCTCCAGAAACACCCACATTACCTGTTCTTCTTGG  
GTAGCTTGTCCATCAGCTCCACGCCCTGTGACACCTTCTGAAGCTGGAGGGCTGGAGAAGGGGGTTGTATTCA  
TCAATGCCAGAACCTTGGACGTTACTGGAACATTGGACCCCAGAAGACGCTTACCTCCAGGTCCCTGGTTGA  
GCAGCGGAATCAACCAGGTCACTGTTTGAGGAGACGATGGGGCCCTGCATTACAGTTCACGGAAACCCCC  
ACCTGGGAGGAACCAAGTACATTAGT**GAGCGGTGGCACCCCTCTGCTGGTCCAGTGGGAGACTGCGCCTC**  
CTCTGACCTGAAGCCTGGCTGTGCCCCACCCCTCACTGCAAAGCATCTCTTAAGTAGCAACCTCAGGG  
ACTGGGGGCTACAGTCTGCCCTGTCTCAGCTAAACCCCTAAGCCTGCAGGGAAAGGTGGATGGCTCTGGGCC  
TGGCTTGTGATGATGGCTTCTCAAGCCCTGCTCTTGCGCAGGCTGTGGCTGTCTCTAGGGTGGGAGC  
AGCTAATCAGATGCCAGCCTTGGCCCTCAGAAAAAGTGTGAAACGTGCCCTGCACGGGACGTACAGCCC  
TGGGAGCATCTGCTGGACTCAGGCGTGCTCTTGCTGGTCCCTGGGAGGCTTGGCACATCCCTCATGGCCCC  
TTTATCCCCGAAATCTGGGTGTGTCACCAGTGTAGAGGGTGGGAAAGGGGTGTCTCACCTGAGCTGACTTGT  
CTTCCCTTACAACCTCTGAGCCTCTTGGGATTCTGGAAGGAACCTGGCGTGAGAAACATGTGACTTCCCTT  
TCCCTCCCACCGTGTCTCCCACAGGTGACAGGCTGGCTGGAGAACAGAAATCCTCACCCCTGCCCTTCC  
CAAGTTAGCAGGTGTCTGGTCTCAGTGAGGAGGACATGTGAGTCTGGCAGAACGCCATGGCCATGTCTGCA  
CATCCAGGGAGGAGGACAGAACGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGGCCATGTCTGACATCC  
AGGGAGGAGGACAGAACGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGGCCATGTCTGACATCCAGGG  
GGAGGGACAGAACGCCAGCTCACATGTGAGTCTGGCAGAACGCCATGGCCATGTCTGACATCCAGGGAGG  
ACAGAACGCCAGCTCAGTGGCCCCCGCTCCCCACCCCCCAGGCCAACAGCAGGGGAGGAGCAGGCCCTCCTTC  
GAAGTGTGTCCAAGTCCGCATTGAGCCTTGTCTGGGGCCCAGGCCAACACCTGGCTTGGCTACTGTCTGA  
GTTGCAGTAAAGCTATAACCTTGAATCACAA

## **FIGURE 64**

MTTWSLRRR PARTLGLLLL VV LGFLV LRR LDW STLVPL RL RQL GLQAK GWN F MLED STFW  
I FGGS I HYFRV PREY WRDR LLK M KAC GLN T LTT YVP WNL H EPERG K FDF SGN LDLE A FV LMA  
AEI GLW VIL R PGP YIC CSEMDL GGL P SWL LQDP GMRL RTTY KGF TEAVD LYFDH LMS R VVPLQ  
YK RGG PII AVQ VEN EYGS YN KDPAY MPYV KKA LEDRG IVE L L TSDN KDG LSK GIV QGV LAT  
INL QSTHE LQ LTTFL FNV QGT QPK MVMEY WTGF DSW GGPH NILD SSEV LKTV SAI VDAG S  
SIN LYMF HGGT NFG FMNG AMHF HDY KSDV TSYD YDAVL TEAGD YTA K YMKL RDFF GSI SGIP  
LPPP P D L L P KMP YEP LTPV LYLS LWDALK YLGE PIK SEK P I N M E N L P VNG GNG QSF GYI LY  
TSIT SSG ILS GHV H D RGQ V FV NTV S I GFL DYK TTKIA VPLI QGYTV L RIL VEN RGRV NYGEN  
ID DQRK GLI GNLYL ND SPL K N FRI Y S L D M K K SFF QRF GLD K W X S L P E T P T L P A F F L G S L S I S  
S T P CDTFL KLEG W EKG VV FING QNL GRY W N IGP QK TLYL PGP WLSS GIN QV I V F E E T M A G P A  
LQFTETPHLGRNQYIK

**Signal sequence:**

amino acids 1-27

**Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

**N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

## **FIGURE 65**

GGGGACGCGGAGCTGAGAGGCCTCGGGCTAGCTAGGTGTAGGGTGGACGGGTCAGGACCG  
CTGGTGAGGGTTCTACTTGGCCTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG  
GGAGCAAAAGCCGGCTCGGCCGAGGCCCGAGGACCTCCATCTCCAATGTTGGAGGAATC  
CGACACGTACGGCTGTCAGACTAGAGGAGCCGTAAACGCCATGGCTCCC  
AAGAAGCTGTCCTGCCTCGTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA  
GGCAGACACTCGGTGTTGTTAGGGTCAAGGGTCTGACCGGTTCTCTAGACGGGCCC  
CGTTCCGCTATGTGTCTGGCAGCCTGCACTACTTCGGTACCGCGGTGCTTGGCCGAC  
CGGCTTTGAAGATGCGATGGAGCGGCCCAACGCCATACAGTTTATGTGCCCTGGAACTA  
CCACGAGCCACAGCCTGGGTCTATAACTTAAATGGCAGCCGGACCTCATTGCCCTTCTGA  
ATGAGGCAGCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTACATCTGTGAG  
TGGGAGATGGGGGTCTCCCATCCTGGTGTGAAACCTGAAATTCAAGAACCTC  
AGATCCAGACTTCCTGCCGAGTGGACTCCTGGTCAAGGTCTGCTGCCAAGATATATC  
CATGGCTTATCACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC  
TACAGAGCCTGTGACTCAGCTACATGAGGCACGGCTGGCTGGCTTCCGTGCACTGCTAGG  
AGAAAAGATCTGCTCTTACACAGATGGGCTGAAGGACTCAAGTGTGGCTCCCTCCGGG  
GACTCTATACCACTGTAGATTGGCCAGCTGACAACATGACCAAAATCTTACCCGTCTT  
CGGAAGTATGAACCCCAGGGCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA  
CTGGGGCCAGAACATCCTCCACAGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC  
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG  
AATGGTGCCGATAAGAAGGGACGCTTCCCGATTACTACCAAGCTATGACTATGATGCACC  
TATATCTGAAGCAGGGGACCCACACCTAACGCTTTGCTCTCGAGATGTCACTGCAAGT  
TCCAGGAAGTCCTTGGACCTTACCTCCCCGAGCCCCAAGATGATGCTGGACCTGTG  
ACTCTGCACCTGGTGGCATTACTGGCTTCTAGACTTGCTTGGCTGGGGCCAT  
TCATTCAATCTGCCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGTACC  
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGTGCCTAACATAATGGAGTC  
CATGACCGTGCCTATGTGATGGTGGATGGGTGTTCCAGGGTGTGGAGCGAAATATGAG  
AGACAAACTATTTGACGGGAAACTGGGTCAAACCTGGATATCTTGGTGGAGAACATGG  
GGAGGCTCAGCTTGGGTCTAACAGCAGTGAATTCAAGGGCTGTTGAAGCCACCAATTCTG  
GGCAAACAATCCTTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTGTGAAGTG  
GTGGTTTCCCTCCAGTTGCCAAATGGCCATATCCTCAAGCTCCTCTGGCCCCACATTCT  
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG  
ACCAAGGGCAAGTCTGGATCAATGGTTAACGGCCGGTACTGGACAAAGCAGGGGCC  
ACAACAGACCCCTACGTGCCAAGATTCTGCTGTTCTAGGGAGCCCTCAACAAAATTA  
CATTGCTGGAACCTAGAAGATGTACCTCTCCAGCCCCAAGTCAAATTGGATAAGCCTATC  
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG  
TGCCTCTGAACCAATGGAGTTAAGTGGCACTGAAAGTAGGCCGGCATGGTGGCTCATGC  
CTGTAATCCCAGCAGTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA  
CCAGCCTGCCAACATGGTAAACCCCGTCTCCACTAAAAATACAAAATTAGCCGGCGTG  
ATGGTGGGCACCTCTAACCTCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTGAATCC  
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA  
GACACTCCATCTCAAAAAAA

## **FIGURE 66**

MAPKKLSCIRSLLLPLSLTLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL  
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE  
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF  
TLLRKYEPHGPLVNSEYYTGWLWQGNHSTRSVSAVTKGLENMLKLGASVNMYMFHGGTNF  
GYWNGADKKGRFLPITTSDYDAPISEAGDPTPKLFALRDVISKFQEVPPLGPLPPSPKMML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN  
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRSLFGSNSSDFKGLLKP  
PILGQTIILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL  
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLSDTLSASEPMELSGH

**Signal sequence:**

amino acids 1-27

**N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

**Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

**Tyrosine kinase phosphorylation site.**

amino acids 191-198

**N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## **FIGURE 67**

GCTTGAAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTGC  
ACCCACAATATGGCTTACATGTTAAAAAGCTCTCATCAGTTACATATCCATTATTGTGT  
TTATGGCTTATCTGCCTCTACACTCTTCTGGTTATTCAAGGATACCTTGAAGGAATATT  
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAAACGATTT  
GCGTTCCCTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT  
CTTGTCAAGAGTTAGTGAAAATAACTTAGGAAATTAGTTGAACCATGAGTGGACATTG  
AAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG  
CTGTCGGGGGTGCCGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC  
AATTCCAGAAGCTAAAATTCTGCTAAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC  
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTGAGA  
TGCCTTCACGTGAAGAGTTCACTGATGTGGCTGAAATTCTGCCTGGGTGTATTGCTCAAAA  
CCTTCGAGAGAGTTGTACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT  
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC  
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCCAGA  
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAATTACAGGAACGGAT  
TTAAAGTCCAATAACATTGCACAATTGAGGAAATCATCAGTTCCAGCATTTAAAACGACT  
GACTTGTAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTATTACCCATGTCA  
AAAACTTGGAGTCACTTATTCTCAACAAAGCTCGAACCTTACCGAGTGGCAGTATT  
AGTTACAGAAAATCAGATGCTTAGATGTGAGCTACAACAAACATTCAATGATTCCAATAGA  
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC  
CAAAACAATTGTTAAATGCATAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC  
TCACCTCCAGAGAAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG  
CTTGGACCGCCTGCCAGCCCCAGCTGGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGG  
TGGAAAGATCACCTTTGATACCCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA  
AATATTCCCTTGCAAATGGATTTAACTAAGATAATATATGCACAGTGATGTGCAGGAAC  
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG  
ATACATCTTTAAAATAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT  
GTTCAATGTTGTAGGGTTAAAGTCATTCCAAATCATTGTTTTCTTTGGGG  
AAAGGGAAGGAAAATTATAATCACTAATCTGGTTCTTTAAATTGTTGTAACGGAT  
GCTGCCGCTACTGAATGTTACAAATTGCTGCCTGCTAAAGTAAATGATTAAATTGACATT  
TTCTTACTAAAAAAAAAAAAAA

## **FIGURE 68**

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL  
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG  
VPDAVFDLTDLDVLKLELIELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH  
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMICLQELSLRELRHLKILHVKSNLTKVPSN  
ITDVAPHLTKLVIHNDGKLLVNLNSLKKMMNVAELELQNCERIPHAIFSLSNLQELDLKS  
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ  
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTILNLGQNCITSLP  
EKVGQLSQLTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP  
FANGI

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

**Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

**Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

**N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

## **FIGURE 69**

## **FIGURE 70**

MELVRRLMPLTLLILSCLAEILTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ERPENKSIRIIFSYVQLDPDGSCESENIKVFDGTSSNGPLLQVCSKNDYVPVFESSSTLT  
FQIVTDSARIQRTVFVFFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV  
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVPTFESSNSLTVVLS  
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP  
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST  
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN  
LVVFLDTCRASPTDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNFKFLRSMSSVYL  
QCKVLICDSSDHQSRCNQGCVRSKRDIISSYKWKTDIIIGPIRLKDRSASGNSGFQHETHA  
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

**Signal sequence:**

amino acids 1-24

**Transmembrane domain:**

amino acids 571-586

**N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

**Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

**N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 71**

GACGGAAGAACAGCGCTCCCGAGGCCGCGGAGCCTGCAGAGAGGACAGCCGGCTCGCGCG  
GGACATGCGGGCCCCCAGGAGCTCCCAGGCTCGCGTCCCGTTGCTGCTGTTGCTGC  
TGCTGCCGCCGCCGTGCCCTGCCACAGGCCACGCCCTCGACCCCACCTGGGAGTCC  
CTGGACGCCGCCAGCTGCCCGCGTGGTTGACCAGGCCAAGTCGGCATCTTCATCCACTG  
GGGAGTGTGTTCCGTGCCAGCTCGGTAGCGAGTGGTCTGGTGGTATTGGCAAAGGAAA  
AGATAACCGAAGTATGTGAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT  
TTTGGACCACATTACAGCAAATTAAATGCCAACCCAGTGGGCAGATATTTCAGGC  
CTCTGGTGCCAAATACATTGCTTAACCTCAAACATCATGAAGGCTTACCTTGTGGGGGT  
CAGAATATTGTTGAACTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA  
CTTGAGGTAGCCATTAGAACAGAACTGACCTGCGTTGGACTGTACTATTCCCTTTGA  
ATGGTTTCATCCGCTTCTGAGGATGAATCCAGTTCAATTCCATAAGCGGCAATTTCAG  
TTTCTAAGACATTGCCAGAGCTATGAGTTAGTGAACAACATCAGCCTGAGGTTCTGTGG  
TCGGATGGTGACGGAGGACCCGATCAATACTGGAACAGCACAGGCTTGGCTGGTT  
ATATAATGAAAGCCCAGTCGGGGCACAGTAGTCACCAATGATCGTGGGAGCTGGTAGCA  
TCTGTAAGCATGGTGGCTCTACCTGCAGTGTATACCCAGGACATCTTGCA  
CATAAATGGAAAATGCATGACAATAGACAAACTGTCCTGGGTATAGGAGGGAGCTGG  
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTCATGTG  
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTCTGTAGTTTGAG  
GAGCGACTGAGGCAAGTGGGTCTGGCTAAAGTCATGGAGAAAGCTATTATGAAACCTA  
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG  
AAAAATTAGTCTATGCCATTAAATGGCCCACATCAGGACAGCTGGCTGGCCAT  
CCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGCCATGGACAGCCACTTAAC  
GATTCTTGAGCAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCATCAGATGC  
CGTGTAAATGGGGCTGGCTAGCCCTAACTATGTGATCTAAAGTGCAGCAGAGTGGCTG  
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA  
AAGCAATGAAACTGGATAAGAAAATTATTGGCAGTTCCAGCCCTTCCCTTTCCACTA  
AATTTTTCTTAAATTACCCATGTAACCATTAACTCTCCAGTGCACCTTGCCTAAAGTC  
TCTTCACATTGATTGTTCCATGTGACTCAGAGGTGAGAATTTCACATTATAGTAG  
CAAGGAATTGGTGGTATTATGGACCGAACATGAAAATTATGTTGAAGCCATATCCCCCATG  
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAAATGCATTGCTAGTCAT  
TTTTTTGTGCCAACATCATAGAGGTGATTACAAAATCCTAGATGGCATAGCCTACTACA  
CACCTAATGTGTATGGTATAGACTGTTGCTCTAGGCTACAGACATATAACAGCATGTTACTG  
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATGAAACATATGAAACATAGAGAAG  
GTACAGTAAAATACTGTAAAATAATGGTGACCTGTATAGGGCACTTACCCAGAATGGAG  
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA  
TTGAACACTGCCAGACGTTAAAATACTGTATGCTTAGGCTACACTACATTATAAAAAAAA  
GTTTTCTTCTTCAATTATAAACATAAGTGTACTGTAACCTTACAAACGTTTAATT  
TTTAAACCTTTGGCTTTGTAATAACACTTAGCTAAAACATAAAACTCATTGTGCAA  
ATGTAA

## **FIGURE 72**

MRPQELPRLAFPLLLLLLPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIFHWG  
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS  
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLFEW  
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETY  
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

**Signal sequence:**

amino acids 1-28

**N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

**Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

**Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

**N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

**Leucine zipper pattern.**

amino acids 410-432

**Alpha-L-fucosidase putative active site.**

amino acids 283-295

## **FIGURE 73**

AGCAGGGAAATCCGGATGTCTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT  
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATTGCCCTCATATCACCAAGTGGCCATC  
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGCCAGGTGCTTCAGCCTGGTGTG  
CTTCTCACTTCCATCTGGACCACGAGGCTCTGGCCAAGGCTCTTGCCTGCAGAAGAGCT  
TTCCATCCAGGTGTCTGCAGAATTATGGGGATCACCCCTGTGAGCAAAAGGCGAACAGC  
AGCTGAATTTCACAGAAGCTAAGGAGGCCTGAGGCTGCTGGACTAAGTTGGCCGGCAAG  
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAAACTTGAGCTATGGCTGGGTTGGAGA  
TGGATTCTGGTCATCTCTAGGATTAGCCAAACCCCAAGTGTGGAAAAATGGGGTGGGTG  
TCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACATCTGAT  
ACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCA  
AACTGCAACACAAACACAAGAATTATGTCAAGTGACAGTACCTACTCGGTGGCATCCCTT  
ACTCTACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGG  
AGAAAAAAATTGATTGTGTCAAGAAGTTTATGAAACTAGCACCATGTCTACAGAAAC  
TGAACCATTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTC  
CCACGGCTCTGCTAGTGCTCTCCCTTGGTGTGCAAGCTGGCTTGGATTTC  
TATGTCAAAAGGTATGTGAAGGCCTTCCCTTTACAAACAAGAATCAGCAGAAGGAAATGAT  
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAATGAGGAATCAAAGA  
AAACTGATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCCTGGAA  
GCTGAAGTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC  
TTACCCCTGCCAGCTGGGAAATCAAAGGGCAAAGAACCAAAGAAGAAAGTCCACCCCTT  
GGTCTTAATGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC  
CCTTCTCCTATTGTAACCCTGCTGGATCCTATCCTCTACCTCAAAGCTTCCACGGCC  
TTCTAGCCTGGCTATGCTCTAATAATATCCCACCTGGAGAAAGGAGTTGCAAAGTGCAA  
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTGAGGCTAGG  
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTACTGATTCCGAGCTCAGAC  
CCTTCTCAGCTCTGAAAGAGAAACACGTATCCACCTGACATGTCCTCTGAGCCGGTA  
AGAGCAAAGAATGGCAGAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG  
ACCTAATCTGTAAAGCTAAAATAAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACT  
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTGAAACACATTGAGTTGGA  
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTTCTCT  
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAATTCTATTGTTATCTGA  
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAAGTAATAAAATTCA  
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGCAAGGTATTACACTCTGTAAT  
TGAATATTATTCTCAAAAATTGCACATAGTAGAACGCTATCTGGAGCTATTTCTCA  
GTTTGATATTCTAGCTTACTCTACCTCAAACTAATTCTATTGCTGAGACTAATCTT  
ATTCACTTCTCTAATATGGCAACCATTATAACCTTAATTATTATAACATAACCTAAGAAG  
TACATTGTTACCTCTATATACCAAAGCACATTAAAAGTGCCATTAACAAATGTATCACTA  
GCCCTCCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGACAAAAAATTAA  
AGCATTAGAAAATT

## **FIGURE 74**

MARCFSLVLLLTSIWTTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR  
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNSPKCGKNGVGVLIWKVPVSRQF  
AAWCYNSSDTWTNSCIPETTTKDPFNTQTATQTTEFIVSDSTYSVAPYSTIPAPTTTPP  
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFF  
GAAAGLGFCYVKRYVKAFFPTNKNQQKEMIETKVVKEEKANDSNPNEESKTDKNPEESKSP  
SKTTVRCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## **FIGURE 75**

AGATGGCGGTCTGGCACCTCTAATTGCTCTCGTGTATCGGTGCCGCACTTCACGATGG  
CTCGCCCAACCTTACTACCTTCTGT~~CGGCC~~CTGCTCTGCTGCCCTACTCGT~~GAGGAA~~  
ACTGCCGCCGCTCTGCCACGGTCTGCCACCCAA~~CG~~GAAGACGGTAACCGTGTGACTTG  
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGT~~GCC~~ATTGTGATGATGAAGAACCGCAGA  
TCCATCACTGTGGAGCAACATATAGGCAACATTTATGTTAGTAAAGTGGCCAACACAAT  
TCTTTCTCCGCTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC  
TGATGACGTGCAAACCCCCCTATATATGGCCTGAGTATATCAAGTACTTCATGATAAA  
ACCATTGATGAGGA~~ACTAGA~~ACGGACAAGAGGGTC~~ACTTGGATTGTGGAGTT~~CTTGCCAA  
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC  
GTACAGGGCTAAATTGGAAAGGTGGATGTTGGACGCTACTGATGTTAGTACGGGTAC  
AAAGT~~GAGCACATCACCC~~CTCACCAAGCAACTCCCTACCC~~G~~TAC~~CCTGTT~~CCAAGGTGGCAA  
GGAGGCAATGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTG  
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGGGCCAAGAAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGC~~GTG~~GGCTCAACCCCCACCACAGTGT~~CAG~~  
TGGGAAAACAAGAAGGATAAAAAGATCCT~~ACTTGG~~CAGT~~GCTC~~CTC~~CTGT~~CAATT  
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGC~~CTT~~NATTNATGTTTCC~~CTT~~GG  
CTGNGACTGGNTGGGCCAGCATGCAGCTCTGATTTAAAGAGGCATCTAGGGATTGTCAG  
GCACCC~~T~~ACAGGAAGGC~~TGCC~~ATGCTG~~GG~~CCA~~ACTG~~TTCA~~G~~GGAGCAAGAAAGAGATC  
TCATAGGACGGAGGGAA~~ATGG~~TTCC~~CT~~CCAAGCTGG~~GT~~GT~~TA~~ACTG~~CT~~TATC  
AGCTATT~~CAGACAT~~CTCCATGGTTCTCCATGAA~~ACTCTG~~GGTT~~CATC~~ATT~~CCTCTT~~AG  
TTGACCTGCACAGCTGGTTAGACCTAGATTAA~~CC~~TAAGGTAAGATGCTGGGT~~TAGA~~  
CGCTAAGAATTTC~~CCCC~~CAAGGACT~~CTT~~GCT~~CC~~TTAAGCC~~CT~~GGCT~~CG~~TTATGGTC  
TTCATTAAAAGTATAAGCCTA~~ACTT~~GT~~CG~~CTAG~~T~~C~~TA~~AGGAGAA~~AC~~CTTAA~~CC~~ACAAAG  
TTTTTATCATTGAAGACAATATTGAACAACCCCTATT~~TT~~GT~~GGGG~~ATTGAGAAGGGGT~~GAA~~  
TAGAGGCTTGAGACTTC~~CTT~~GT~~GG~~TAGGACTGGAGGAGAA~~ATCC~~CTGGACT~~TT~~CAC  
TAACCC~~T~~GT~~AC~~ACT~~CCCC~~ACACCC~~AG~~TTGATGG~~CTT~~CG~~TA~~ATAAAAGATTGGATT  
TCCTTTG

## **FIGURE 76**

MAVLAPLIALVYSPVRLSRWLAQPYYLLSALLSAAFLLVRKLPPCHGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL  
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC  
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRACKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

**Signal sequence:**

amino acids 1-48

**Transmembrane domain:**

amino acids 111-125

**N-glycosylation site.**

amino acids 165-169, 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

**Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

**N-myristoylation site.**

amino acids 188-194, 225-231

**Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

## **FIGURE 77**

GGACAGCTCGGGCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGACGTTGCCCTG  
GGGCCCCAGCCTGGCCCGGGTCACCCCTGGCATGAGGAGATGGCCTGTCCTGGTCCCA  
TTGCTCCTGCTGCCGGCTCCTACGGACTGCCCTCTACAACGGCTTCTACTACTCCAACAG  
CGCCAACGACCAGAACCTAGGCAACGGCATGGAAAGACCTCCTAATGGAGTGAAGCTGG  
TGGTGGAGACACCGAGGGAGACCCCTGTTCACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC  
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGGCGTGTGCGTGTCAAATGGTGGAAAGCT  
GTCGGAGAACGGGCCCCAGAGAACGGACGTGCTGGTGGCCATGGGCTGAGGCACCGCTCCT  
TTGGGACTACCAAGGCCGCGTGCACCTGCGCAGGACAAAGAGCATGACGTCTCGCTGGAG  
ATCCAGGATCTGCGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTATTGACGGCTGGAG  
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGGGGGTGTGGTCTTCCTTACCAAGTCCCCCA  
ACGGGCGCTACCAAGTCAACTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCGGTG  
GTGGCCTCCTTGAGCAGCTCTCCGGGCCTGGGAGGAGGGCCTGGACTGGTGCAACCGGG  
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCAGCCCTGCGGTGGCC  
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACCGCCCTGCACCGCTATGAT  
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCTGAGAACGCT  
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGGAC  
AGCTTTGCCGCCTGGAAGTCCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT  
GGCAGCGTCCGCTACCCCTGTGGTCACCCGATCCTAACTGTGGCCCCAGAGCCTGGGT  
CCGAAGCTTGGCTTCCCCGACCCGAGAGCCGCTTGTACGGTGTACTGCTACCGCCAGC  
ACTAGGACCTGGGCCCTCCCGCCATTCCCTACTGGCTGTATTATTGAGTGGTT  
CGTTTCCCTGTGGTTGGAGCCATTAACTGTTTATACTCTCAATTAAATTCT  
TTAACATTTTTACTATTGGTAAAGCAAACAGAACCCAAATGCCCTCCCTTGCTCCTG  
GATGCCCACTCCAGGAATCATGCTGCTCCCTGGCATTGGGTTGTGGCTTCTG  
GAGGGTTCCCCGCCATCCAGGCTGGCTCCCTCCCTTAAGGAGGGTGGTGGCCAGAGTGGG  
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGCATGGTGGCACAGTTCTCCCTGCC  
CAGCCTGGGGAAAGAACGGCCTGGGGCCTCCGGAGCTGGCTTGGCCTCTCCTGCC  
CACCTCTACTCTGTGAAGCCGCTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA  
GCCAGTTCTAGGCTCCAGGCAGGAAATCTGAGGAAAGGAAGAACCTCCCTCCCTG  
TCCCTCTCGGTTCCAAAGAACATGTTGTCATTGTTCTCCTGTTCCCTGTGTGG  
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGTATGACTGCCCTCCGCCAA  
AA  
AA

## **FIGURE 78**

MGLLLVPLLLLPGSYGLPFYNGFYYNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRYRYEPALVSPRRVRVKWWKLENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESLVLELRGVVFYQSPNGRYQFNFHEGQQ  
VCAEQAAVVASFEQLFRAWEEGLDWNCAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSGPR  
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

**Signal sequence:**

amino acids 1-17

**Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

**Tyrosine kinase phosphorylation site.**

amino acids 137-145

**N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

## **FIGURE 79**

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCG**A**TGATGTGGCGACCATCAGTTCTGCTGC  
TTCTGTTGCTACTGAGGCACGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC  
CAGGGGAGGGTGCACCAGGCAGGCCCTGAGCGACGCTCCCCATGATGACGCCACGGGAA  
CTTCCAGTACGACCATGAGGCTTCTGGACGGGAAGTGGCAAGGAATTGACCAACTCA  
CCCCAGAGGAAAGCCAGGCCGTCTGGGCGGATCGGACCGCATGGACCGCGGGGAC  
GGCGACGGCTGGGTGTCGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCAGCGCA  
CATACGGGACTCGGTGAGCGCGGCCCTGGGACACGTACGACACGGACCGCGACGGCGTGTGG  
GTTGGGAGGAGCTGCGCAACGCCACCTATGCCACTACGCCCGGTGAAGAATTTCATGAC  
GTGGAGGATGCAAGAGACCTACAAAAAGATGCTGGCTGGGACGAGCGCGTTCGGGAGG  
CGACCAGGATGGGACTCGATGCCACTCGAGAGGGAGCTGACAGCCTCCTGCACCCCGAGG  
AGTTCCCTCACATGCGGACATCGTATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAA  
GATGGCTATGTCAGGTGGAGGAGTACATCGGGATCTGTACTCAGCCGAGCCTGGGAGGA  
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTCCGGACTTCCGGATCTGAACAAGG  
ATGGGCACCTGGATGGAGTGAGGTGGCCACTGGGTGCTGCCCTGCCAGGACCGAGCCC  
CTGGTGGAAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGGCTGAGCAA  
AGCGGAAATCCTGGTAATTGGAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG  
ACCTGACCCGGCACCAACGATGAGCT**G**GCACCGCGCACCTGCCACAGCCTCAGAGGCCCG  
CACAAATGACCGGAGGAGGGGCCGTGGTCTGGCCCTCCCTGTCCAGGCCCGAGGAG  
GCAGATGCAGTCCAGGCATCCTCTGCCCTGGCTCTCAGGGACCCCTGGTGGCTTC  
TGTCCCTGTCACACCCCCAACCCAGGGAGGGCTGTCATAGTCCCAGAGGATAAGCAATAC  
CTATTCTGACTGAGTCTCCAGGCCAGACCCAGGGACCCCTGGCCCAAGCTCAGCTCTAA  
GAACCGCCCAACCCCTCCAGCTCAAATCTGAGCCTCCACACATAGACTGAAACTCCCCT  
GGCCCGAGCCCTCTGCCCTGGCCTGGCCTGGACACCTCCTCTGCCAGGAGGAATAA  
AAGCCAGCGCCGGACCTTGAAAAA  
AAAAAAAAAAAAA

## **FIGURE 80**

MMWRPSVLLLLLLRHGAQGKPSDAGPHQGRVHQAPLSDAPHDDAHGNFQYDHEAFLGR  
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGVSLAELRAWIAHTQQRHIRDSVSAAWDT  
YDTDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE  
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ  
FRDFRDLNKGHDGSEVGHVLPPAQDQPLVEANHLLHESDTDKGRLSKAEILGNWNMFV  
GSQATNYGEDLTRHHDEL

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 140-144

**Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

**N-myristoylation site.**

amino acids 263-269, 311-317

**Endoplasmic reticulum targeting sequence.**

amino acids 325-330

## **FIGURE 81**

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTGAGCAGGTGCGGAGCCCCGG  
GCGGCGGGCGCGGGTGCAGGGATCCCTGACGCCCTGTCCCTTTGTCGCTCCCAG  
CCTGTCTGTCGTCGTTGGCGCCCCGCCTCCCGCGGTGCGGGGTTGCACACCGATCCTG  
GGCTTCGCTCGATTGCGCCGAGGCGCCTCCCAGACCTAGAGGGCGCTGGCCTGGAGCAG  
CGGGTCGTCTGTGTCTCTCTGCCCTGCGCCGCCGGGATCGAAGGGTGCAGGGCTCT  
GAGGAGGTGACCGCGGGGCCTCCGCACCCCTGGCCTGCCGATTCTCCCTCTCTCCAG  
GTGTGAGCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCCAGCTCTGGCCTCGGTGTG  
TGTCTGCTGCTGCTGCCGGGCGCGGGCAGCGAGGGAGGCCCTCCATTGCTATCACATG  
TTTACAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGCTGCC  
CTCTGAGGAATTCTCTGTGTATGGAACATAGTATATGCTCTGTATCGAGCATATGTGGG  
GCTGCTGTCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC  
TGGTCGAGAAAACATTCTCAGTAGATGCCAATGGCATTCCAGTCTCAAATGCTTTCTAGAT  
GGTCTGCTTCTTCACAGTAACAAAGGAAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCAGAGAAGAAAACGG  
CAATAAAGATTGTAAGCAGACATTGCATTCTGATTGATGGAAGCTTAATATTGGCAGC  
GCCGATTTAATTACAGAAGAATTGTTGGAAAAGTGGCTCTAATGTTGGAAATTGGAACA  
GAAGGACCATGTGGCCTTGTCAAGCCAGTGAACATCCAAAATAGAATTAACTTGAA  
AAACTTACATCAGCAAAGATGTTGTTGCCATAAGGAAGTAGGTTCAAGAGGGGTA  
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA  
GTAAGAAAAGGGATCCCCAAAGTGGTGGTATTATTGATGGTGGCCTCTGATGACAT  
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTGGTGTCAATGTATTAGTTCTGTGGCCA  
AGCCTATCCCTGAAGAACTGGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGTCTGT  
CGGAATAATGGCTTCTCTTACACATGCCAAGTGGTTGGCACCACAAAATACGTAAA  
GCCTCTGGTACAGAAAGCTGTGCACTCATGAACAAATGATGTCAGCAAGACCTGTTATAACT  
CAGTGAACATTGCCCTTCTAATTGATGGCTCCAGCAGTGGAGATAGCAATTCCGCC  
ATGCTTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTCCAAGAT  
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTCAGTTCACTGACTATAGCACCA  
AAAGAGATGTCCTAGCTGTCACTAGAAACATCGCTATATGAGTGGGAAACAGCTACTGGT  
GATGCCATTCTTCACTGTTAGAAATGTTGGCCCTATAAGGGAGAGCCCCAACAGAA  
CTTCCTAGTAATTGTCACAGATGGGCAGTCCTATGATGTCAGGCTCTGGATGACCTG  
CACATGATGCGAGGAATCACTATCTCTGTGGTGTGGCTGGCACCTCTGGATGACCTG  
AAAGATATGGCTCTAACCGAAGGAGTCTCACGCTTCTCACAAGAGAGTTCACAGGATT  
AGAACCAATTGTTCTGATGTCATCAGAGGATTGAGAGATTCTTAGAATCCCAGCAAT  
AATGGTAACATTGACAACTGAAAGAAAAGTACAAGGGATCCAGTGTAAATTGATT  
CTCATAATAGTAAATGCTTACTGATACTAGAATCAGATACAAACTATTAAGTATGTCAAC  
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCCTCTGGTTACAATTACAGTGT  
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAACTCAGGAAAGAGGA  
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAA  
TTCCATAGCTCAATAAGAATCTGATACTTAGACCAAAAAAAA

## **FIGURE 82**

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLEEFSVY  
GNIVYASVSSICGAAVHRGVISSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT  
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCCKADIAFLIDGSFNIGQRRFNLQKN  
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDLFAIKEVGFRGGNSNTGKAL  
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSSDIEEAGIVAREFGVNVFIVSVAKPIPEELG  
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCHEQMMCSKTCYNSVNIAFLI  
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTESFTDYSTKENVLAVI  
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI  
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

**Signal sequence:**

amino acids 1-24

**N-glycosylation site.**

amino acids 100-104, 221-225

**Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532

**N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

**Amidation site.**

amino acids 145-149

### **FIGURE 83**

CGCCCGCGCTCCCGCACCGCGGCCACCGCGCCGCTCCGCATCTGCACCCGCAGGCC  
GGCGGCCTCCGGCGGGAGCAGACAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTC  
GGCGCGGCTCGGGCGCAGAGCGGAGATGCAGCGGCTGGGGCACCTGCTGCGCTGC  
TGCTGGCGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCACCTCGCTCCAGTC  
AAGCCCGGCCGGCTCTCAGTACCCGAGGAGGCCACCTCAATGAGATGTTCCCGA  
GGTTGAGGAACGTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGTGGAAAGAGATGGAGG  
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCAGCTAT  
ACAATGAGACCAACACAGACACGAAGGTTGAAATAATACCATGTCACCGAGAAAT  
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG  
TGGGAGACGAAGAAGGCAGAAGGAGGCCACGAGTGCATCATCAGCAGGGACTGTGGGCCAGC  
ATGTAAGTGCCTTGCAGCTTCCAGTACACCTGCCAGGCATGCCGGGCCAGAGGATGCT  
CTGCACCCGGACAGTGAAGTGTGGAGACCAGCTGTGTCTGGGTCACTGCACCAAAA  
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG  
TGCTGTGCCTTCCAGAGAGGCCTGCTGTTCCCTGTGTGCACACCCCTGCCGTGGAGGGCGA  
GCTTGCCATGACCCGCCAGCCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG  
GAGCCTTGGACCGATGCCCTGTGCCAGTGGCCTCTGCCAGCCCCACAGCCACAGCCTG  
GTGTATGTGTGCAAGCCGACCTCGTGGGAGCCGTGACCAAGATGGGAGATCCTGCTGC  
CAGAGAGGTCCCCGATGAGTATGAAGTGGCAGCTTCACTGGAGGAGGTGCGCCAGGAGCTGG  
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGCTGCCGCT  
GCACTGCTGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTTAGATGTGCAATAGAA  
ATAGCTAATTATTCAGGTGTGCTTAGGCGTGGCTGACCAAGGCTCTTCTACA  
TCTTCTTCCCAGTAAGTTCCCTGTGGCTGACAGCATGAGGTGTGTCATTGTCAGC  
TCCCCCAGGCTGTTCTCAGGCTTCAGTCTGGTGTGGAGAGTCAGGCAGGGTTAAC  
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACAGTTGGCAG  
ACAGCCGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGAAACAATGTGG  
AGTCTCCCTGTGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAAAACATCAA  
CCTGGAAAAATGCAACAAATGAATTTCACGCACTTCCATGGCATAGGTAAGCTG  
TGCCTTCAGCTGTTGAGATGAAATGTTCTGTCACCCGATTACATGTGTTATTCTAC  
AGCAGTGTGCTCAGCTCCTACCTCTGCCCCAGGGCAGCATTTCATATCCAAGAGTCAATT  
CCTCTCTCAGCACAGCCTGGGGAGGGGTCAATTGTTCTCCTCGCCATCAGGGATCTCAGAG  
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACAGAGCAGTTCT  
CTGGTTGTGACTCTAACGCTCAGTGCTCTCCACTACCCACACCGCTTGGTGCACCAA  
AAGTGTCCCCAAAAGGAAGGAGAATGGGATTTTCTTGAGGCATGCACATCTGAAATTAG  
GTCAAACTAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTC  
AGTGTGGGGAGCCGCTTCTAATGAAGACAATGATATTGACACTGTCCTCTTGGCAGT  
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATAAGGTTAACCTGCAGAAACA  
GTACTTAGGTAATTGTAGGGCGAGGATTATAATGAAATTGCAAAATCACTTAGCAGCAAC  
TGAAGACAATTATCAACCAACGCTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGT  
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTCAGGTGTCA  
TGGACTGTTGCCACCATGTATTCCAGAGTTCTTAAAGTTAAAGTTGACATGATTGTA  
TAAGCATGTTCTTGAGTTAAATTATGTATAAACATAAGTGCATTAGAAATCAAGC  
ATAAAATCACTCAACTGCAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 84**

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ  
HKLRSAVEEMEAEEAAKASSEVNLANLPPSYHNETNTDTKVGNNNTIHVHREIHKITNNQTG  
QMVFSETVITSVGDEEGRRSHECI IDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG  
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGGLCCAFQRGLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV  
GSFMEEVRQELEDLERSLTEEMALGEAAAAALLGEEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

## **FIGURE 85**

AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCTG  
AAGATAACAATAATTCACTCCACTCTCCCTCCAAACACACATGTGATGTACACACACACATACA  
CACACATAACACTTCCTCTCCTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACAC  
TAAAGCCTTAAGGACAGGCTGGCCATTACCTCTGCAGCTCTGGCTGTGAGTCAAAAAACATGGGAGGG  
CCAGGCACGGTACTCACACCTGTAATCCCAGCATTGGGAGACCGAGGTGAGCAGATCACTGAGGTCAAGGAG  
TTCGAGACCAGGCTGGCAACATGGAGAAACCCCCATCTACTAAAAATACAAAAATTAGCCAGGAGTGGTGGC  
AGGTGCCTGTAATCCCAGTACTCAGGTGGCTGAGCCAGGAGAATCGCTGAATCAGGAGGCGGAGGATGCAGT  
CAGCTGAGTCACCGCTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACACGGGAGGA  
GGGGTAGATACTGCTCTGCAACCTCCCTTAACCTGCACTCTCTTCCAGGCTGCCCTGATGGGCGCTG  
GCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGAAGGCAATTGAGGAGGGCAAGAAGTGA  
GTGAGAATGACTGCCCTGGGAGGGTGGTCTGGGCCCTGGCAGGGTGTGACCCCTGCAAACACA  
AAGACAGGACTCCAGACTCCCTTGTGAATGGTCCCTGGCAGCTCCACCATGAGGCTTCTCGTGGCCCC  
ACTCTTGTAGCTTGGTGGCTGTGCACTGCCCCGTGTTACCGCCCTGGCATGTCCTGCCCCCTCA  
GTGTGCCCTGCCAGATCCGCCCTGGTATAACGCCCTGTCCTACCGCAGGACTTACCTGTGGACTGCAATGA  
CCTATTCCCTGACGGCAGTCCCCCGCACTCCCCCGCAGGACACAGACCTGTCAGAGAACAGCATTGT  
CCGTGTGGACCAGAGTGAAGCTGGGCTACCTGGCAATCTCACAGAGCTGGACCTGTCAGAACAGCTTCGGA  
TGCCCGAGACTGTGAATTCCATGCCCTGCCAGCTGCTGAGCCTGACACTAGAGGAGAACAGCTGACCGGCT  
GGAGGACCACAGCTTGCAGGGCTGCCAGCCTACAGGAACCTATCTCAACCACAACCAGCTTACCGCAGC  
CCCCAGGGCTTCTGGCTCAGCAACTTGTGCTGCGGCTGACCTCAACTCCAACCTCTGAGGGCATTGACAG  
CCGCTGGTTGAAATGCTGCCAACCTGGAGATACTCATGATTGGCGGAACAAGTAGATGCCATCTGGACAT  
GAACCTCCGGCCCTGGCAACCTGCGTAGCCTGGTGTAGCAGGATGAACCTGCGGAGATCTCCGACTATGC  
CCTGGAGGGCTGCAAAGGCTGGAGAGCCTCTCTTCTATGACAACCAGCTGGCCGGGTGCCAGGCGGCACT  
GGAACAGGTGCCGGCTCAAGTCTAGACCTCAACAAGAACCCGCTCCAGGGTAGGGCCGGGGACTTGC  
CAACATGCTGACCTTAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTGCCCTGGT  
GAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCCTTCATCCACCCCCCGCCTTCCA  
CCACCTGGCCCCAGATGGAGACCCCTCATGTCACAAACAACGCTCTGAGTGGCTTGCACCAGCAGGGTGGAGTC  
CCTGGCCAACCTGCAAGGGTAGGTCTCCACGGCAACCCCATCCGCTGTGACTGTGTCATCCGCTGGCCAATGC  
CACGGGCACCGTGTCCGTTCATCGAGCCGAATCCACCTGTGTGGAGCCTCCAGCAGCCTCCC  
GGTCCTGAGGTGCCCTTCCGGAGATGACGGACACTGTTGCCCTCATCTCCCCACGAAGCTTCCCCAAG  
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTGCAATTGCCGGCACTGGCGAACCCGAACCCGAGATCTACTG  
CGTCACTCCAGCTGGCTCGACTGACACCTGCCATGCAAGCAGGAGGTACGGGTACCCCGAGGGACCC  
GGAGCTGCCAGGGTGACAGCAGAACAGAGGCAAGGGCTATACACCTGTGTCCTGCCAGAACCTGGGGCTGACAC  
TAAGACGGTTAGTGTGGTTGTGGGCGTGTCTCTCCAGCCAGGCAAGGAGCAGGGCTGGAGCTCC  
GGTCAGGAGACCCACCCCTATCACATCTGCTATCTGGTCACCCACCAACAGTGTCCACCAACCTCAC  
CTGGTCCAGTGCCTCCCTCCCTCCGGGCCAGGGGCCACAGCTCTGCCCTGCCCTGGGAACCCACAGCTA  
CAACATTACCCGCCCTCTCAGGCCACGGAGTACTGGGCCCTGCAAGTGGCCCTTGCTGATGCCACACCCA  
GTTGGCTGTGATGGGCCAGGACCAAGAGGGCAACTCTTGCACAGAGCCTTAGGGGATGTCCTGGCTCAT  
TGCCATCTGGCTCTCGCTGTGCTTCTCTCCAGCTGGGTTCTGGGCTGGAGTGCCTTCTGTCGGTTGT  
GGGTGTGGGTGGAGGCGGCCCTCCCTCCAGCTGGGTTCTGGGCTGGAGTGCCTTCTGTCGGTTGT  
GTCTGCTCCCTCGTGTGCTGCCCTGGAAATCCAGGGAGGAAGTGCCTCAGAGAACACTAGGACTACTTTTACCAA  
ACCATTTGTCTCAAATTCTTGAAGCTCAAGCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTACCAA  
AGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGGACCCACGTGCTTGAGGGCTGGCAGCTGGC  
CAAGACAGATGGGGCTTGTGGCCCTGGGGTGTCTCTGCAGCCTGAAAAAGTGCCTTACCTCTAGGGTCA  
CCTCTGCTGCCATTCTGAGGAACATCTCAAGGAACAGGAGGGACTTGGCTAGAGCCTCTGCCCTCCCATCTT  
CTCTCTGCCAGAGGCTCTGGGCTGGCTTGCTGCCCTACCTGTGTCCTCCGGCTGCCACCCCTTCCCTT  
TCTTTCTCTGTAAGTCTCAGTTGCTTGCTCTGTGCTGCCCTGGCAAGGGCTGAAGGAGGCACACTCCATCTCAC  
CTCGGGGGCTGCCCTCAATGTGGAGTGACCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAA  
CGCTCATCTCAGCAGCTGGCTGGCAITCCGAAGCTGACTTTCTATAGGCAATTGTACCTTGTGGAGAA  
ATGTGTCACTCCCCAACCCGATTCACTCTTCTCTGTAAAAAATAAAAATAATAACAATAAAA  
AAAA

## **FIGURE 86**

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA  
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDSQNSFSDARDCDFHALPQLLSLHL  
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILDMNFRPLANLRSVLVAGMNLREISDYALEGLQSLSESLSFYDNQ  
LARVPRRALEQVPGLKFLDLNKNPLQRVPGDFANMLHLKELGLNNMEELVSIDKFALVNLP  
ELTKLDITNNPRLSFIHPRAFHHLQMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIR  
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPLQ  
VASGESMVLHCRALEPEPEIYWVTPAGLRLTPAHGRRYRVYPEGTLELRRVTAAEAGLYT  
CVAQNLVGADETKTVVVGRALLQPGRDEGQGLELRVQETHPYHILLSWTPPNTVSTNLTW  
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS  
CHRALGDRPGLIAILALAVLLAAGLAHLGTGQPRKGVGGRRLPPAWAFWGWSAPSVRVV  
SAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 629-648

**N-glycosylation site.**

amino acids 94-98, 381-385, 555-559, 583-587

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 485-489

**Casein kinase II phosphorylation site.**

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

**Tyrosine kinase phosphorylation site.**

amino acids 532-540

**N-myristoylation site.**

amino acids 15-21, 493-499, 566-572

**Amidation site.**

amino acids 470-474, 660-664, 692-696

## FIGURE 87

GCAAGCCAAGGCGCTTTGAGAAGGTGAAGAAGTCCGGACCCATGTGGAGGAGGGGACATTGTGTACCGCCT  
CTACATGGCGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA  
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGCTACCGCACCTACCGCTGTGCCACCC  
CCTGGCCACACTCTCAAGATCCTGGCTCCTCTACATCAGCCTAGTCATCTCTACGGCCTCATCTGCATGTA  
CACACTGTGGTGGATGCTACGGCGTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGAGAGCAGCTACAG  
CGACATCCCCGACGTCAAGAACGACTTCGCGCTCATGCTGCACCTCATTGACCAATACGACCCGCTACTCCAA  
GGCGCTTCGGCTCTCTGCGAGGTGAGTGAGAAGCTGGCGAGCTGAACCTCAACAAACGAGTGGACGCT  
GGACAAAGCTCCGGCAGGGCTCACCAAGAACGGCAGGACAAGCTGGAGCTGCACCTGTTCATGCTCAGGGCAT  
CCCTGACACTGTGTTGACCTGGAGCTGAGGCTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCGCC  
CAGCATTGCCAGCTCACGGCCTCAAGGAGCTGGGCTTACACACAGGGCAAGATTGAAGGCCCTGCGCT  
GCCCTTCCTGCGGAGAACCTGGGGCGTGCACATCAAGTTACCGACATCAAGGAGATCCGCTGTGGATCTA  
TAGCTGAAGACACTGGAGGAGCTGCACCTGACGGCAACCTGAGGGAGAACACCGCTACATCGTCATCGA  
CGGGCTGGGGAGCTCAAACGCTCAAGGTGCTGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCAC  
AGATGTGGCGTGCACCTGAGAACGCTGTCATCAACAATGAGGGACCAAGCTCATCGTCCTCAACAGCCTCAA  
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCACCTGGAGCGATCCCCACTCCATCTCAGCCT  
CCACAACTGCAAGGAGATTGACCTCAAGGACAACACCTCAAGGACATCGAGGAGATCATCAGCTTCCAGCACCT  
GCACCGCTCACCTGCTTAAGCTGGTACAACACATCGCCTACATCCCCATCCAGATGGCAACCTCACCAA  
CCTGGAGGCCCTACCTGACCCACAACAAACCTGACCTTCCCTGGCGACATCGGCTCTGCGAGAACCTCCAGAACCT  
CTACCTGGGACCTCAGCCACAACAAACCTGACCTGGAGCTCTCCAGTGGCGAGCTGACCAACCTGACGAGATCGAGCTGGGG  
AGCCATCACGGCAACCGGATCGAGACGCTCCCTCCGGAGCTCTCCAGTGGCGAGCTGACCAACCTGACGAGATCGAGCTGGGG  
GGGGCAACAACTGCTGCTGAGTCAGTGCCTCCAGGGTGGCGAGCTGACCAACCTGACGAGATCGAGCTGGGG  
CAACCGGGCTGGAGGTGCTGCTGGAGCTGGCGAGTGGCCACTGCTCAAGCGCAGCGGCTGGTGGAGGAG  
GGACCTGTTCAACACACTGCCACCCCAGGTGAAGGAGCGCTGTGGAGGGCTGACAAGGAGCAGGCCAGCGAG  
GCCGGCCAGCACAGCAAGCAGCAGGACCGCTGCGCTGGCAGGAGCCTGGGGCGCTTGTGAGTCAGGCCAGAGCAGA  
AACTCCCGACAGCCAGGACAGCCTCGCGCTGGCAGGAGCCTGGGGCGCTTGTGAGTCAGGCCAGAGCAGA  
GGACAGTATCTGTGGGCTGGCCCTTTCTCCCTCTGAGACTCACGCCCCAGGGCAAGTGTGTTGGAGGAG  
AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGCTCCCTCCCTGGAGGCCAGCTGCCCCAGGGCTGAG  
CTGCCACAGAGGTCTGGGACCTCACTTTAGTTCTGGTATTATTTATTTCTCATCTCCACCTCCTCATCC  
AGATAACTTATACATTCCAAGAAAGTTCAGCCAGATGGAAGGTGTTCAAGGGAAAGGTGGGCTGCCCTTCC  
TTGTCCTTATAGCGATGCCCGGGGCAATTAAACACCCATCTGGAGACTTCAGCAGAGTGGTCCGGGGCAACCCAG  
CCATGGGACGGTCAACCGAGTGGGGCTCTGGCTCTGGAGCTGGCAGTGGTGGAGACTTTGGTGGGGTATTAA  
AAGGCCAGGCTGGAGCTGGCTCTGAGTTGGAGCTTCAGGGCAGGGTGGCAGTTCCCTGAGCAAAGCAGGCCAGGT  
AAAAGACACTAACGGCCAGTGGAGCTCAGGGCAGGGTGGCAGTTCCCTGAGCAAAGCAGGCCAGGT  
TGAAGTGTGTTCTCCCTGGGCGCAGGGTGTCTCCGGATCTGGTGTGACCTGGTCCAGGAGTT  
CTATTTGTTCTGGGAGGGAGGTTTTTGTGTTGTTGGTTTTGGGTTTTGGGTGTTCTGTTCTTCTCC  
ATGTCGCTTGGCAGGCACTCATTCCTGTCGGCTGTCGGCAGAGGGAAATGTTCTGGAGCTGCCAAGGAGGGAG  
ACTCGGGTTGGCTAATCCCCGGATGAACGGTGTCCATTGCAACCTCCCTCCCTGGCTGCCCTGCCCT  
CGCACAGTGTAAAGGAGCCAAGAGGGAGCCACTTCGCCCCAGACTTTGTTCTCCCACTCCCTGGGCAATGGGTGTT  
CCAGTGGCCACCGCTGGCTCCGCTGCTTCATCAGCCCTGCGCACCTGGCTTCTCATGAAGAGCAGACACTTA  
GAGGCTGGTGGGAATGGGAGGTGGCCCTGGAGGGCAGGCGTTGGTCAAGCCGGTTCCGTCCCTGGCGC  
CTGGAGTGCACACAGCCAGTGGCACCTGGTGGCTGGAGCCAACCTGCTTGTAGATCACTCGGGTCCCCACCTT  
AGAAGGGTCCCCGCTTAGATCAATCACGTGGACACTAAGGCACGTTAGAGTCTTGTCTTAATGATTATGT  
CCATCCGCTGTCCGTCATTGTGTTCTGCGTCGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG  
CCTCTGACAACCATGAAGCAAAATCGTTACATGTGGGTCTGAACCTGAGACTCGGTACAGTATCAAATAAA  
ATCTATAACAGAAAAAAAAAAAAAA

## **FIGURE 88**

MRQTIICKVILIIICYTVYYVHNIFDVDCVDIESLTGYRTYRCAHPLATLFKILASFYI  
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSIDPDVKNDFAFMLHLIDQYDPLYSK  
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLELHLFMLSGIPDVTVDLVELEV  
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFTDIKEIPLWI  
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVRLKSNLSKLPQVVTDVGVLQKLSI  
NNEGTLKLVNLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ  
HLHRLTCLKLWYNHIAYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT  
FLPADIGLLQNLQNLAITANRIETLPPPELFQCRKLRALHGNVQLQSLPSRVGELTNLTQIE  
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

**Transmembrane domain:**

amino acids 51-75 (type II)

**N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

**Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

**N-myristylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

## **FIGURE 89**

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCAATGGAGCTGGCACTGCGGCGCTCTCCCGT  
CCCGCGGTGGTTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCAATTGACT  
GGCCCACAGAGGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG  
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACCTCTCAGAACTGCCCTGGTCAT  
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGC  
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT  
GTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA  
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTCAGTTGCCACAAAG  
AATTCCAGACAGTCCATTCTACATTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCGAGGGACCATCAAGTGAACCTTGCGGGGGT  
TGCCTGGGTGATTCTGGATCTCCCCTGTTGATTGGTGCCTCCTGGGACCTTACCTGT  
ACAGCATGTCTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA  
CTGAATGCCGTAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT  
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAGCACTCCA  
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTGTCTTGTAGCGC  
CACGTGAGACACCTACAACGAGATGCCCTAACGAGCTCATGAATGCCCATCAGAAAGAA  
GCTCAAAATTATTCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTGTGAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC  
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATAACATGGGTCAAGGAGGCCTG  
GGTGGGAAACTGAAGTGGCCAGAACTGCCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCCCTGT  
ACAGTGACCCCTAAATCTTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTT  
TACTGGATTCTGAAAGCTGGTCATATGGTCTCTGACCAAGGGACATGGCTCTGAAGAT  
GATGAGACTGGTACTCAGCAAGAATGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT  
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT  
AACTGGGCTGTGATCAAGAAGGTTCTGACCAGCTCTGCAGAGGATAAAATCATTGTCTCT  
GGAGGCAATTGGAAATTATTCGCTTCTTAAAAACCTAAGATTTTAAAAAATTGAT  
TTGTTTGATCAAAATAAAGGATGATAATAGATATTAA

## **FIGURE 90**

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLANVNKGLYRE  
ATELWGKAEMIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS  
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP  
SDQGDMALKMMRLVTQQE

**Signal sequence:**

amino acids 1-25

**N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

**Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

**N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

## **FIGURE 91**

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCTC  
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCAGGCCGTTATCAGGACCATGCGGCCGA  
CGGGTCATCACGTCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA  
GGGGAGCCTGCGCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG  
CACTCACGGCGCGCACTGCTTGAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG  
GTCCAGTTGGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG  
TTACTCGTATCGAATATCTATCTGAGCCCTCGTACCTGGGAATTACCCCTATGACATTG  
CCTTGGTGAAGCTGTCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG  
GCCTCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA  
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAAGTCAGGTGCCATCAAACA  
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG  
GTTTGTGCTGGCAACGCCAACGGGGAGGATGCCCTGCTCGGTGACTCAGGTGGACCCCTT  
GGCCTGTAACAAGAATGGACTGTTGATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG  
GTCGGCCAATCGGCCGGTGTCTACACCAATATCAGCCACCACTTGGATCCAGAAG  
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGCCACTACTCTTTCCCTCT  
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCATGCAGCCTGGGC  
CACTGCCAAGTCAGGCCCTGGTTCTTCTGTCTTGGTAATAAACACATTCCAGTTGA  
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 92**

MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW  
DSHVCGVSLLSHRWALTAAHCFETYSSDLSDPSGWMQFGQLTSMPSFWSLQAYYTRYFVSNI  
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP  
SPHTLQEJVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG  
LWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL  
LGPV

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

**Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

**N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

**Amidation site.**

amino acids 33-37

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

**Serine proteases, trypsin family, histidine active site.**

amino acids 78-84

## **FIGURE 93**

CCCCACCGCGTCCGGGACCGTGGGAAGGGCAGA**ATGGGACTCCAAGCCTGCCTCTAGGGCT**  
CTTTCGCCCTCATCCTCTGGCAAATGCAGTTACAGCCGGAGCCGACCAGCGGAGGACGC  
TGCCCCCAGGCTGGGTGTCCTGGCCGTGGACCCCTGAGGAAGAGCTGAGTCACCTT  
GCCCTGAGACAGCAGAATGTGAAAGACTCTGGAGCTGGTGAGGCTGTGAGTCACCTT  
CTCTCCTCAATACGGAAAATACCTGACCCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC  
CACTGACCCCTCACACGGTGCAGGGAAACCCATGGCTCTGGCAGCCAGAAGTGCCT  
GTGATCACACAGGACTTCTGACTTGCTGGTGAGCATCCGACAAGCAGAGCTGCTGCT  
TGGGCTGAGTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTGTAAGGTCCCCAC  
ATCCCTACCAGCTCCACAGGCCTGGCCCCCATGTGGACTTTGTGGGGGACTGCACCGT  
TTTCCCCAACATCATCCCTGAGGCAACGTCCCTGAGCCGAGGTGACAGGGACTGTAGGCCT  
GCATCTGGGGTAACCCCTCTGTGATCCGTAAGCGATAACAACCTGACCTCACAAGACGTGG  
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCCCTGGAGCAGTATTCCATGAC  
TCAGACCTGGCTCAGTTCATGCGCCTCTCGGTGGCAACTTGCACATCAGGCATCAGTAGC  
CCGTGTGGTGGACAACAGGGCCGGGGCCGGGATTGAGGCCAGTCTAGATGTGCACT  
ACCTGATGAGTGTGGTGCACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGATGAG  
GGACAGGAGCCCTTCCTGCAGTGGCTCATGCTCAGTAATGAGTCAGCCCTGCCACATGT  
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCCCTACATCCAGCGGGTCA  
ACACTGAGCTCATGAAGGCTGCCCTGGGGTCTCACCTGCTCTCGCCCTAGGTGACAGT  
GGGGCCGGGTGTTGGTCTGTCTGGAAAGACACCAGTTCCGCCCTACCTTCCCTGCCCTCAG  
CCCCTATGTCACCACAGTGGAGGCACATCCTCCAGGAACCTTCCATCACAATGAAA  
TTGTTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTTCCCACGGCCTTCATACCAGGAG  
GAAGCTGTAACGAAGTTCTGAGCTCTAGCCCCCACCTGCCACCATCCAGTTACTTCATG  
CAGTGGCGTGCCTACCCAGATGTGGCTGCACCTCTGATGGCTACTGGTGGTCAGCAACA  
GAGTGCCCATTCATGGGTGTCCGGAACCTCGGCCTCTACTCCAGTGTGTTGGGGATCCTA  
TCCTTGATCAATGAGCACAGGATCCTAGTGGCCGCCCCCTCTGGCTTCTCAACCCAAG  
GCTCTACCAGCAGCATGGGCAGGTCTCTTGATGTAACCGTGGCTGCCATGAGTCCTGTC  
TGGATGAAGAGGTAGAGGGCAGGGTTCTGCTCTGGCTGGATCCTGTAACAGGC  
TGGGGAACACCAACTTCCAGTTGCT**GAAGACTCTACTCAACCCCTGACCCCTTCATC**  
AGGAGAGATGGCTGTCCCTGCCCTGAAGCTGGCAGTTCACTCCCTATTCTGCCCTGTTG  
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA  
TGCTGTGAGCTTGACTTCACTCCACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT  
CCTGCCCTAGATTCTCAATAAGATGCTGTAACTAGCATTGATGAAATGCCCTCCCTCCGC  
ATCTCATCTTCTCTTTCAATCAGGCTTCCAAAGGGTTGTATAACAGACTCTGTGCACTA  
TTTCACTGATATTCACTCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT  
TTCCTACCCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTGCTTATG  
GCCTTCCATCATAGTTGCCCACTCCCTCTCCTACTTAGCTCCAGGTCTAACCTCTTG  
ACTACTCTTGTCTCCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTCATTG  
TCCATTGCTAGATTTGCTCTCAGTTACTCATTGTCCTGGAACAAATCACTGACA  
TCTACAAACCATTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATAACCTCAA  
TGTAAAAAA

## **FIGURE 94**

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSLTFALRQQNVERLS  
ELVQAVSDPSSPQYGKYLTLENVALVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL  
SIRQAEELLPGAEFHYYGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPTSSLRQRP  
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYILMSAGANISTWVYSSPGRHEGQEPFLQWLM  
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAARGLTLFASGDGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVPRPSYQEEAVTKFLSSSP  
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG  
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPSQLC

**Signal sequence:**

amino acids 1-16

**N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

**Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

**Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

**N-myristoylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

## **FIGURE 95**

GGCGCGCGCTCTCCGGCGCCACACCTGTCTGAGCGCGCAGCGAGCCGGCCGGC  
GGGCTGCTCGCGCGGAACAGTGCTCGC**ATGG**CAGGGATTCCAGGGCTCCTTCTC  
TTCTTCTGCTCTGTGCTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTG  
GCCTGCATACCGCCTCCCTGCGTCTGCCCCAGTCTACCCCTCAATTAGCCAAGCCAGACT  
TTGGAGCCGAAGCAAATTAGAAGTATCTCTTATGTGGACCCCAGTGTATAAGGAACT  
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTATGCCAATGG  
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC  
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC  
AGGTTCAGCATTGGAAAGGACTTCCTGCTCAACTACCCTTCTCAACATCAGTGAAGTT  
ATCCACGGGCTGCACCGCACCCCTGGCAGAGAACATGTCCCTCACAGCTGCCACTGCA  
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTCGAGTGGCTTCTAAAGCCC  
AAGTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCGAGCAGATGAA  
ATTCAGTGGATCCGGGTGAAACGCACCCATGTGCCAAGGGTTGGATCAAGGGCAATGCCA  
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACCTAAAAGCCCCACAAGAGAAAA  
TTTATGAAGATTGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGGCAGAATTCACTTCTC  
TGGTTATGACAATGACCGACCAGGCAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA  
CCTATGACTTGCCTACAGCAATGCGATGCCAGCCAGGGGCCAGGGGTCTGGGTCTAT  
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGAGCGAAAAATTATTGGCTTTTCAGG  
GCACCAAGTGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAATCACTC  
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGGG  
**TGAC**CACAGTGTCCCTCCTGGCAGCAATTAGGGTCTTCATGTTCTTATTAGGAGAGGCC  
AAATTGTTTGTCTGGCGTGCACACGTGTGTGTGTGTGTAAAGGTGT  
CTTATAATCTTTACCTATTCTACAATTGCAAGATGACTGGCTTACTATTGAAAATG  
GTTTGTGTATCATATCATATATCATTAAAGCAGTTGAAGGCATACTTTGCATAGAAATAA  
AAAAAAACTGATTGGGCAATGAGGAATATTGACAATTAGTTAATCTCACGTTTG  
CAAACTTGATTTTATTCATCTGAACTTGTTCAAAGATTATTAATATTGGCATA  
CAAGAGATATGAAAAA

## **FIGURE 96**

MAGIPGLLFLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLQSTLNLA  
KPDFGAEAKLEVS  
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTEQVGIYILSSSGDGAQHRD  
SGSSGKS  
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKH  
VLTAACIHDGKTYVK  
TQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHV  
PKGWIKGNANDIGMDYD  
YALLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNL  
VYRFCDVKDETYDLLYQQCD  
AQPGASGSGVYV  
RMWKRQQQKWERKIIIGIFSGHQW  
VDMNGSPQDFN  
AVRITPLKYAQICYW  
IKGNYLDCREG

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 93-97, 207-211

**Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

**Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

**N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

**Serine proteases, trypsin family, histidine active site.**

amino acids 171-177

## **FIGURE 97**

GCATGCCCTGGGTCTCTGAGCCTGCTGCCCTGCCCTCCCCCCCCACCAGCCATGGTGGTTT  
CTGGAGGCCCCAGCCCTGGGTGGGGCTGTCTCGCACCTCACCTCCCTGCTGCTGCTG  
GCGTCGACAGCCATCCTCAATGCGCCAGGATACTGTTCCCCAGCCTGTGGGAAGCCCCA  
GCAGCTGAACCGGGTTGTGGCGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAATGGGACCCACCACACTGCCAGGTTCTCTGCTCACCAAGCCCTGGGTGATC  
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACTGTTCTGTGCTGCTGGG  
GGCCTGGCAGCTGGGAACCCCTGGCTCTCGTCCCAGAAGGTGGGTGTTGCCTGGTGGAGC  
CCCACCCCTGTGTATTCTGGAAGGAAGGTGCCGTGCAGACATTGCCCTGGTGCCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGCCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT  
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTCCCTTGC  
CCCACCCCTCAGACCCCTGCAGAAGCTGAAGGTTCTATCATGACTCGGAAGTCTGCAGCCAT  
CTGTACTGGCGGGGAGCAGGACAGGGACCCCATCACTGAGGACATGCTGTGCCGGCTACTT  
GGAGGGGGAGCGGGATGCTTGTCTGGCGACTCCGGGGCCCCCATGTGCCAGGTGGACG  
GCGCCTGGCTGCTGGCGGCATCATCAGCTGGGCAGGGCTGTGCCAGCGAACAGGCC  
GGGGTCTACATCAGCCTCTCGCGACCGCTCCTGGGTGGAGAAGATCGTCAAGGGTGCA  
GCTCCGGCGCGCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCC  
CCCGCGCGCTCCTAGGGCGCAGCGGGACGCCGGCTCGGATCTGAAAGGCGGCCAGATCCACA  
TCTGGATCTGGATCTGGCGGGCTCGGGCGTTCCCGCCGTAAATAGGCTCATCTACC  
TCTACCTCTGGGGCCCGGACGGCTGCTGGGAAAGGAAACCCCTCCCCGACCCGCCCCGAC  
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCGCCAACGGCCTCATGTCCCCGCCCCAC  
GACTTCCGGCCCCGCCCGGGCCCCAGCGCTTTGTGTATATAATGTTAATGATTTTAT  
AGGTATTGTAACCCTGCCAACATATCTTATTATTCCCAATTCAATAATTATTATT  
CTCCAAAAAA

## **FIGURE 98**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFSTSLLLASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLDPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGII SWGEGCAERNRPGVYISLSAHR SWEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS
```

**Signal sequence:**

amino acids 1-32

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

## **FIGURE 99**

GACGGCTGCCACCATGCACGGCTCCTGCAGTTCTGATGCTCTGCTGCCGCTACTGCTA  
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTGATGGT  
GGAGCTGCACAACCTCTACCGGGCCAGGTATCCCCACGGCCTCACAGACATGCTGCACATGA  
GATGGGACGAGGAGCTGGCCGCCTCGCCAAGGCCTACGCACGGCAGTGCCTGGGGCAC  
AACAAAGGAGCGCGGGCGCGCGAGAACTGTTGCCATCACAGACGAGGGCATGGACGT  
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAAACCTCAGGCCGCCACCT  
GCAGCCCAGGCCAGATGTGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC  
GGCTGTGGTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT  
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC  
CGTGCCTCCAAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC  
CCGGAAGATGCTCAGGATTGCTTACCTGGTAAGTGGCCATCCTCCGGCGACTGA  
AGCATCAGACTCTAGGAAAATGGGTACTCCTCTCCCTAGCAACGGGATTCCGGTTTCT  
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCCTGCTGTGAAACCCAGGCC  
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTGCGTAAC  
AACTGAGGTCCCTCCATTGGCAGCTCACAGCCTGCCCTCCCTGGATGAGGAGGCCAGTTA  
CCTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA  
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTGGACCCCAAGATGTCCCTGACAGGGCAAG  
GGAACCTCCTACCCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCAGTG  
AGGTCTTGGCCTCAGTTTCCAGGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC  
CACACGGGGCACACCTCCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA  
TGCCACGGGTGGCGTGCCCTGGCTCTGCAGTCGTCCTGCCAGGTGCAGAGGCCCTGACA  
AGCCTAGCGTTGTGTCAAGGGCTGAACCTGGCCCTGGTCATGTGTGGGCCCTCCTGGGA  
CTACTGCTCCTGCCTCCTGGTGTGGCTGGAATCTTCTTGAATGGATACCAACTCAAAGGG  
TGAAGAGGTCACTGTCTCTGTCACTCTCCCCACCCCTGTCCCCAGCCCTAAACAAGATA  
CTTCTGGTTAAGGCCCTCGGAAGGGAAAGGCTACGGGCATGTGCCTCATCACACCCTCC  
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC  
GGGCCACACCTCTCCTGCCCTCCCTGGTGTGGCTGGAATCTTCTTGAATGGATACCAACTCAAAGGG  
CACTGCCCTACCTGGCTGGGCTGTCTGCCACACAGCATGTGCCTCTCCCTGAGTGCCTG  
TGTAGCTGGGATGGGATTCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTTC  
TTTGAGTGGGGAGGCAGGGACGAGGAAGGAAAGTAACCTGACTCTCCAATAAAAACCT  
GTCCAACCTGTGAAA

## **FIGURE 100**

MHGSCSFLMLLLPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPtasDMLHMRWDEE  
LAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ  
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC  
PSGYHCKNSLCEPIGSPEADAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV  
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKS  
THVPIPKSADKVTDKTKVPSRSPENSMDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS  
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV  
SGLNSGPGVWGPLLGLLLPPLVLAGIF

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

## **FIGURE 101**

GTAACCTGAAGTCAGGCTTTCATTTGGGAAGCCCCCTCAACAGAACCGGACTATTCTCCAAGTTATGGTGGACGT  
ACTTCTGTTGTTCTCCCTCTGTTGCTTTTACACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTCAT  
CAAGGCAGTTCCATGAGCCACCTTCAAAGCCTCGAGAAGTGAACAGTGAACAACAATGAATTGGAGACCATCC  
AAATCTGGGACCAGCTCGGCAAATATTACACTTCTCCTGCTGGAAACAGGATTGTTGAAATACTCCCTGA  
ACATCTGAAAGAGTTCAGTCCTGAAACTTGGACCTTAGCAGCAACAATATTCAAGAGCTCCAAACTGCATT  
TCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGTATTTGACAA  
TTTGGCCAACACACTCCTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCAAGAGATGTTAAACT  
GCCCAACTGCAACATCTGAATTGAACCGAAACAAGATTAAGATGGACTGACATTCCAAGGCCTGG  
TGCTCTGAAGTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAA  
CATGGAAATTTGAGCTGGACCATAACAACCTAACAGAGATTACCAAGGCTGGCTTACGGCTGCTGATGCT  
GCAGGAACCTCATCTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAAGCTCAG  
TGAGCTGGACCTAACCTCAATCAAGGTTAGATGATTCAAGCTCCTGGCTAACGTTACTAAATAC  
ACTGCACATTGGAAACAACAGAGTCAGCTACATTGCTATTGCTGCCTCCGGGGCTTCCAGTTAAAGACTTT  
GGATCTGAAGAACATGAAATTCTCTGGACTATTGAAGACATGAATGGTGTCTTCTGGGCTTGACAAACTGAG  
GCGACTGATACTCAAAGGAAATCGGATCGTTCTATTACTAAAAAGCCTCACTGGTTGGATGCATTGGAGCA  
TCTAGACCTGAGTGACAACGCAATCATGCTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAATT  
GCATTTAAATACATCAAGCCTTGTGCGATTGCCATCCTCAGCTAAAATGGCTCCACAGTGGTGGCGAAAACAACCT  
TCAGAGCTTGTAAATGCCAGTTGTGCCATCCTCAGCTAAAAGGAGAAGCATTGGCTGTAGCCAGA  
TGGCTTGTGTGATGATTTTCCAAACCCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTT  
CAATTGAGTTTCTGCTCAGCTGCCAGCAGTGTGATTCCCAATGACTTTGCTTGAAAAAAAGACAATGA  
ACTACTGCAATGATGCTGAAATGAAATTATGACACACCTCCGGCCCAAGGTGGCGAGGTGATGGAGTATAC  
CATCCTCGGCTGGCGAGGGAAATTGCCAGTGAGGGAAATATCAGTGTGTATCTCAATCACTTGGTC  
ATCCTACTCTGCTAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCAACAGACCCCCATGGATCTCACCAT  
CCGAGCTGGGCCATGGCACGCTGGAGTGTGCTGCTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA  
TGGGGCACAGACTCCCAGCTGCACGGAGAGACGCATGCAATGTGATGCCGAGGATGACGTGTTATCGT  
GGATGTGAAGATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTCAGCAAATGC  
AACTCTGACTGCTCTAGAAACACCATCATTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGC  
CGTCTACAGTGCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACCTGGACCAAAAGATGATAGCCCATTGGTGG  
AACCGAGAGGCACTTTTGCACTGCCAGGAATCAGCTCTGATTATGTGGACTCAGATGTCACTGATGCTGGAA  
ATACACATGTGAGATGCTAAACACCTTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCCAC  
CTGCGACTCCCCCTCAGATGACAGGCCATCGTAGACGATGACGGATGGGCCACTGTTGGGTGCTGATCATAGC  
CGTGGTTGCTGTGGGGCACGTCACTCGTGTGGGTGATCATATACACACAAAGGGGGAGGAATGAAGA  
TTGCAGCATTACCAACACAGATGAGACCAACTTGCAGCAGATATTCTCTAGTTGTCACATCTCAGGTGCTGG  
AGCTGACAGGCAGGATGGGTACGTGCTTCAGAAAGTGGAAAGCCACCCAGTTGTCACATCTCAGGTGCTGG  
ATTTTCTTACCAACACATGACAGTAGTGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAGCTGC  
CACAGATCTGTTCTTGTCCGTTGGATCCACAGGCCATTGATTTGAAGGGAAATGTGATGGCTCAGA  
TCCTTTGAAACATATCATACAGGTTGCAGTCTGACCCAAGAACAGTTTAATGGACCAACTATGAGCCAGTT  
CATAAAGAAAAGGAGTGCTACCCATGTTCTCATCTTCAAGAACATCTGCAGACGGAGCTTCAGTAATATAC  
GTGGCCTCACATGTGAGGAAGCTACTAACACTAGTTACTCTACAATGAAGGACCTGGAATGAAAATCTGT  
TCTAAACAAGTCCTTTAGATTTAGTGCACCATCCAGAGCCAGCGCTGGTTGCCCTCAGTAATTCTTCATGG  
TACCTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTCAGCC  
AAGAGCCTTTATTGAAAGCTCATTCTCCCCAGACTTGGACTCTGGTCAAGAGGAAGATGGAAAGAAAGGAC  
AGATTTCAAGGAAGAAAATCACATTGTACCTTAAACAGACTTAAAGAAACTACAGGACTCCAAATTTCAGTC  
TTATGACTTGGACACATAGACTGAATGAGACCAAAGGAAAGCTTAACATACTACCTCAAGTGAACCTTTTATT  
AAAGAGAGAGAATCTTATGTTTAAATGGAGTTATGAATTAAAGGATAAAATGCTTATTATACAGAT  
GAACCAAATTACAAAAAGTTATGAAATTAAACTCTGGAAATGATGCTCATATAAGAACATACCTTTTAAACTA  
TTTTTAACTTGTATTGCAAAAGTATCTACGTAATTAAATGATATAATCATGATTATTTATGTATT  
TTATAATGCCAGATTCTTTATGGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCATTT  
TTAAATAGAAGTTACTCATTATATTGACACATTATTTAATAAAATGTCATTTGAA

## **FIGURE 102**

MVDVLLLFLSLCLLFHISRPDLSHNRLSFIKASSMSHLQLSLREVKLNNNELETIPNLGPVSAN  
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP  
GYFDNLANTLLVLKLNRRNRISSAIPPKMFKLQLQHLELNRKIKNVDGLTFQGLGALKSLKM  
QRNGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWE  
FCQKLSLELDLTFNHLSRLDDSSFLGLSLLNNTLHIGNNRVSYIADCAFRLSSLKTLDLKNNE  
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSIKKRAFTGLDALEHLDLSDNAIMSLQGNAFSQ  
MKKLQLQHLNTSSLCDQCLKWLPQWVAENNQSFVNASCAPQLLKGRSIFAVSPDGFVCD  
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQG  
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVAKLTVNMLPSFTKTPMDLTIRAGA  
MARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCAQN  
SAGSISANATLTVLETPSFLRPLLDRVTKGTAVALQCIAGGSPPPQLNWTKDDSPLVVTER  
HFFAAGNQLLIVDSDVSDAGKYTCMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLLLLDG  
WATGVVIIAVVCCVVGTSLVWVVIYHTRRNEDCSITNTDETNLPADIPSYLSSQGTLLAD  
RQDGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEATDLFLCPFLGSTGP  
MYLKGNVYGSDFETYHTGCPDPRTVLMHYEPSYIKKKECYPCHPSEESCERSFSNISW  
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA  
YSSFGQPSDCQPRAFYLKAHSPDLDGSEEDGKERTDFQEENHICTFKQTLINYRTPNFQS  
YDLDT

**Signal sequence:**

amino acids 1-19

**Transmembrane domain:**

amino acids 746-765

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## **FIGURE 103**

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGGTGGCTTGCAAAATG  
AAGGATGCAGGACGCAGCTTCTCCTGGAAACCGAACGCAATGGATAAAACTGATTGTGCAAGAGAAGGAAGAAC  
GAAGCTTTCTTGAGCCCTGGATCTAACACAAATGTGTATGTGACACACAGGGAGCATTCAAGAATGAAA  
TAAACCAAGAGTTAGACCCGCGGGGTTGGTGTCTGACATAAATAATAATCTAACAGCTGTTCCCCCTCC  
CCACCCCCAAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCAAAAGAAAAAGTATGTTCATTTCTC  
TATAAAGGAGAAAGTGAGCCAAGGAGATATTTGGAAATGAAAAGTTGGGCTTTTAGTAAAGTAAAGAACT  
GGTGTGGTGGTGTTCCTTCTTTGAATTCCCACAAGAGGAGAGGAAATTAAATAACATCTGCAAAGAAA  
TTTCAGAGAAGAAAAGTGTGACCGCGGAGATTGAGGCATTGATTGGGGAGAGAACCCAGCAGAGCACAGTTGA  
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCGAGTTGGATTTCATCAACCTCCTTTTTAAAT  
TTTATTCCCTTTGGTATCAAGATCATGCGTTCTTGTTCTAACACCTGGATTCCATCTGGATGTTGCT  
GTGATCAGTCTGAAATACAACGTGTTGAATTCCAGAACGGACCAACACCAGATAAATTATGAATGTGAACAAGAT  
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCCTATTGACCCCTGCTTGTGGTGT  
GCTGGCTCTCAACTTCTGTTGGCTGGTCTGGTGGCTCAGACCTGCCCTCTGTGTGCTCCTGCAGCAA  
CCAGTTCAAGGTGATTGTTGGCTGGAAAAACCTGGTGGAGGTTCCGGATGGCATCTCCACCAACACCGCT  
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTCAAGCACTTGAGGCACTGGAAATCCT  
ACAGTTGAGTAGGAACCATATCAGAACCCATTGAAATTGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA  
ACTCTTGAACATCGTCTTACCATCCGAATGGAGCTTTGTAACTGTCTAAACTGAAGGGAGCTCTGGT  
GCGAAACAACCCATTGAAAGCATCCCTTCTTATGCTTTAACAGAATTCCCTTCTGGCGCAGACTAGACTTAGG  
GGAATTGAAAAGACTTTACATACATCTCAGAAGGTGCTTGAAGGTCTGTCACCTGAGGTATTGAAACCTTGC  
CATGTGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAACATGAGCTGGATCTTCTGGGAATCA  
TTTATCTGCCATCAGGCCTGGCTTTCCAGGGTTGATGACCTTCACAAACTGTGGATGATACTGCCCAGAT  
TCAAGTGAATTGACCGAATGCCATTGACAAACCTTCAGTCAGTCAGTGAGGATCAACCTGGCACACAATAATCTAAC  
ATTACTGCCCTCATGACCTCTTCACTCCCTGCACTCATCTAGAGCGGATACATTACATCACAAACCTTGGAACTG  
TAACGTGACATACTGTGGCTCAGCTGGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCCCTG  
TAACACTCCCTCCAACTCTAAAGGGGAGGTACATTGGAGAGCTGACCAGAAATTACTCACATGCTATGCTCCGGT  
GATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTCAGGAGCTGAGCTGAAATGTCGGGCTCCACATC  
CCTGACATCTGTATCTGGATTACTCCAATGGAACAGTCAGTCAGACACATGGGGCTACAAAGTGGGATAGCTGT  
GCTCAGTGTGATGGTACGTTAAATTCTACAAATGTAACGTGCAAGATAACAGGCATGTACACATGTATGGTGAAGTAA  
TTCCGTTGGAAACTACTGTGTTAGCCACCTGAAATGTTACTGCAAGCAACCAACTACTCTTCTTCTTACTTT  
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGGATGAGGCACGGACCAAGATAACAAATGTGGGTCCCACCTCC  
AGTGGTCAGTGGGAGACCAATGTCAGGACCTCTCAGGACATGGGATCCAGGAATTGAGGTCAAGAGACTACCAAAATCATCAT  
CACCACATCCAGTGAATGATATAAACAGTGGGATCCCAGGAATTGAGGTCAAGAGACTACCAAAATCATCAT  
GGGTGTTGTGGCATCACACTCATGGCTGCACTGAGTGTGCTGTCATTCTACAAAGATGAGGAAGCAGCACCA  
TCGGCAAAACCATCACGCCAACAGGACTGTTGAATTATTAATGTGGATGAGATTACGGAGACACACC  
CATGGAAAGCCACCTGCCATGCTGCTATGAGCATGAGCACTAAATCACTATAACTCATACAAATCTCCCT  
CAACCACACAACAGTTAACACAATAATTCAATACACAGTTCAAGTCAACAAAACAAACATCAAAAAAA  
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAAAACAAACATCAAAAAAA  
GACAGTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTGTTCAAAAAGTGTCTTTACAAAAAAACAA  
AAAAGAAAAGAAATTATTATTAAAAATTCTATTGTGATCTAAAGCAGACAAAAAA

## **FIGURE 104**

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVPDGISTNTRLLNLHENQIQIIVKNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPLSLRRLDLGELKRLS  
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHHNPWNCNCIL  
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTGMAAE  
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGN  
TTASATLNTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ  
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN  
HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYNNSYKSPFNHTTVNTINSIHSS  
VHEPLLIRMNSKDNVQETQI

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537

## **FIGURE 105**

## **FIGURE 106**

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELQPSGVAEARPCPTTCRCLGDLDCSR  
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT  
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY  
FDNLANTLLVTKLNRRNRIASIPPKMFKLPQLQHLELRNRIKKNVDGLTFQGLGALKSLKMQR  
NGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAIRISPAWEFC  
QKLSELDLTFNHLRSRLDDSSFLGLSLLNTHIGNNRVSYIADCAFRLGSSLKTLIDLKNNEIS  
WTIEDMNGAFSGLDKLRRLILQGNRIRSIKKRAFTGLDALEHLDLSDNAIMSLQGNAFSQMK  
KLQQLHLNTSLLCDCQLKWLQPQVAENNQSFVNASCAPQLLKGRSIFAVSPDGFVCCDF  
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQGGE  
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVAKLTNVNMLPSFTKTPMDLTIRAGAMA  
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA  
GSISANATLTVLETPSFLRPLLDRTVTGETAVLQCIAGGSPPPKNWTKDDSPLVTERHF  
FAAGNQLLIIVDSDVSDAGKYTCMSNTLGETERGNVRLSVIPTPTCDSPQMTAPSLLDDGWA  
TVGVVIIAVVCCVVGTSLVVVVIIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTLADQ  
DGYVSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEATDLFLCPFLGSTGPMY  
LKGNVYGSDFETYHTGSPDPRTVLMDHYEPSYIKKKECYPCHPSEESCERSFSNISWPS  
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS  
SFGQPSPDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEEHICTFKQTLENYRTPNFQSYLDLT

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 808-828

**N-glycosylation site.**

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

**Glycosaminoglycan attachment site.**

amino acids 886-890

**Casein kinase II phosphorylation site.**

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

**Tyrosine kinase phosphorylation site.**

amino acids 667-675

**N-myristoylation site.**

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

**Leucine zipper pattern.**

amino acids 58-80, 65-87

## **FIGURE 107**

CAAAACTTGCCTCGCGGAGAGCGCCAGCTGACTGAATGGAAGGGCCCGAGCCCGGGAGCGCAGCTGAGAC  
TGGGGGAGCGCTTCCGGCTGTGGGGCGCCGCTCGGCAGGGGGAGCAGGGAAAGGGAGCTGTGGCTG  
CTGCTCCACGAGGCCACTGGTGTGAACCGGGAGAGCCCTGGGTGCTCCCTATCCCTCTTATATA  
GAAACCTTCCACACTGGGAAGGCAGCGCGAGGGCTATGGTGAGCAAGGAGGCCGCTGATCTGCAG  
GCGCACAGCATTCCGAGTTACAGATTACAGATACCAAAATGGAAGGGCAGGAGGAGCAGAACAGCCTGCTGGT  
TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTGAGGCACCATGGCCAGAGCCGGTGTGC  
TGCTCCTGCTGCTGCCACAGCTGCACCTGGACCTGTGCTTGGCTGAGGGCCCCAGGATTGGCGAA  
GTGGCGGCCACAGCCTGAGCCCGAAGAGAACGAAAGAACGAAAGGGCTGCTGGTACTGAGCCCTGAGG  
AGCCCCGGCCTGCCAGCCCGTCACTGCCCCGAGACTGTGCTTCCAGGAGGGCTGCTGGACTGTG  
GCGGTATTGACCTGCGTGAGTTCCGGGGACCTGCTGAGCACACCAACCACCTATCTCTGAGAACAAACCAGC  
TGGAAAAGATCTACCCCTGAGGAGCTCTCCGGCTGACCGGCTGGAGACACTGAACCTGAAACAAACCAGC  
CTTCCCGAGGGCTCCAGAGAACGGCTTGAGCATCTGACCAACCTCAATTACCTGACTTGGCAATAACAAGC  
TGACCTTGGCACCCCGCTTCTGCCAAACGCCGATCAGTGTGGACTTTGCTGCCAACTATCTCACCAAGATCT  
ATGGGCTCACCTTGGCCAAGAACGCAAACCTTGAGGTCTGTGTACCTGACAACAACAAAGCTGGCAGACGCCGGC  
TGCCGGACAACATGTTAACGGCTCCACCAACGTCGAGGTCTCATCTGTGCCAGCAACTTCCGGCCACGTGC  
CCAAGCACCTGCCGCTGCCCTGTACAAAGCTGCACCTCAAGAACAAACAGCTGGAGAACGATCCCCCGGGCCT  
TCAGCGAGCTGAGCAGCTGGCGAGCTATACTCTGACAAACAACTACCTGACTGAGGAGGGCTGGAACACGAGA  
CCTTCTGGAAGCTCTCAGCCTGGAGTACCTGGATCTGCTCAGCAACAAACCTGTCCTGGGCTCCAGCTGGCTGC  
CGCGCAGCCTGGTGTGCTGCACTTGGAGAACGACAGCCATCAGGAGCTGGAGCAGCAATGTGCTGACCCCCATCC  
GCAGCCTGGAGTACCTGCTGCTGCAACAGCAACCAAGCTGGAGGAGCAGGCATCCACCCACTGGCTTCCAGGGC  
TCAAGCGGTGCAACAGGTGACCTGTACAACAAACCGCTGGAGCGCTGCCCCAGTGGCTGCTGCCGCTG  
GCACCCCTATGATCCTGACAACCAACGATCACAGGCATTGGCCCGAAGACTTTGCCACCACTACTCTGGAGG  
AGCTCAACCTCAGCTACAAACCGCATCACAGGCCACAGGTGACCGCGAGCCTCCGCAAGCTGCGCTGCTGC  
GCTCGTGGACCTGTGGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCCCTGAAATGTCATGTGCTGAAGG  
TCAAGCGCAATGAGCTGGCTGCCCTGGCACAGAGGGCGCTGGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA  
CCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCGTGCCCTGGGACCTGCCATCTGAGCTGCTGGACA  
TCGCCGGAAATCAGCTCACAGAGATCCCCGAGGGCTCCCCAGTCACTTGAGTACCTGTCAGAACAAACA  
AGATTAGTGCCTGGCCCAATGCCCTGACTCCACGCCAACCTCAAGGGATCTTCTCAGGTTAACAAAGC  
TGGCTGTGGCTCCGTGGACAGTGCCTCCGGAGGCTGAAGCACCTGCAGGTCTGGACATTGAAGGCAACT  
TAGAGTTGGTGACATTCCAAGGACCGTGGCCGCTGGGAAAGGAAAGAGGAGGAGGAAGAGGAGGAGGAGG  
AGGAAGAGGAAACAAGATAGTACAAGGTGATGCAAGATGTGACCTAGGATGATGGACCGCCGACTTTCTGC  
AGCACACGCCCTGTTGCTGAGCCCCCACTCTGCCGTGCTCACACAGACACACCCAGCTGCAACACATGAGGCA  
TCCCACATGACACAGGGCTGACACAGTCTCATATCCCACCCCTGCCACGGCGTGTCCACGGCCAGACACATGC  
ACACACATCACACCCCTCAAACACCCAGCTCACGCCACACACAACCTACCCCTCCAAACCAACACAGTCTCTGTCACAC  
CCCCACTACCGCTGCCACGCCCTGTAATCATGCAAGGGAGGTCTGCCCTGGCACACACAGGCC  
TTCCCTCCCCCTGTCGACATGTGATGCTGTCATACACACACACACATGCAACAGTCACTGTGCGAA  
CAGGCCCTCAAAGCTATGCCACAGACAGCTCTGGCCAGGAGAATCAGGCCATAGCAGCTGCCGTGCTGCC  
GTCCATCTGCTCCGTCCGTTCCCTGGAGAACACAAAGGTATCCATGCTCTGTGGCCAGGTGCTGCCACCC  
GGAACTCACAAAGCTGGTTTATTCTTTCCCTATGGGACAGGAGCTTCAAGGACTGCTGGCTGGCC  
TGGCCACCCCTGCTCCAGGTGCTGGCAGTCACCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA  
CAGGCACTTTCCAATGGCAAGGCCAGTGGAGGAGGGATGGAGAGGCCCTGGGTGCTGCTGGGGCTGGGG  
CAGGAGTGAAGCAGAGGTGATGGGCTGGGCTGAGGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGAACACCTTT  
GTTCTCAGGCCTGTGGGGAGTCCGGTGTGCTTTTATTTTATCTTTCTAAGGAAAAAAATGATAAAAT  
CTCAAGCTGATTCTTCTGTTATAGAAACAACTAATATAAAAGCATATCCCTATCCCTGCAAAAAAA

## **FIGURE 108**

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHSLSPPEENFAEEEPVLVLSPEEPGPAAVSCP RD CACS QEGVVDGGIDLREFPGDLP  
EHTNHLQLQNNQLEKIYPEELSRLHRLETLNQNNRLTSRGLPEKA FEHTNLNYLYLANNK  
LT LAPRFLPNALISVDFAANYLTKIYGLTFQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV  
EV LILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN  
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSDANVLTPIRSLEYLLLHSN  
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLP RRVRTLMILHNQITGIGREDFATTYF  
LEELNLSYNRITS PQVHRDAFRKLRLRSIDL SGNRLHTLPPGLPRNVHVLKVKRNEAALA  
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDASF RRLKHLQVLDIEGNLEFGDISKD  
RGRLGKEKEEEEEEEEEEETR

Signal sequence:  
amino acids 1-48

N-glycosylation site.  
amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.  
amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.  
amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.  
amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

## **FIGURE 109**

GGGAGGGGGCTCCGGCGCCGCAGCAGACCTGCTCCGGCCGCGCCTCGCCGCTGTCTCCGGAGCGGCAG  
CAGTAGCCCGGGCGGCAGGGCTGGGGGTTCTCGAGACTCTCAGAGGGCGCCCTCCATCGGCCACCAACCC  
CAACCTGTTCTCGCGCCACTCGCCTCGGCCAGGACCCCTGCCCACATGGATTCTCTGGCGCTGGT  
GCTGGTATCCTCGCTTACCTGCAGGGCGCCGAGTCAGGGAGGTGGCCAGGAAATAGTGTATCGAT  
TGGCCTATGCTTATGGTGGAGGATTGACTGCTGCTGGGGCTGGGCTGCCAGTCTTGGGGACAGTGTCAAGCC  
TGTGTGCCAACCACGATGCAAACATGGTGAATGTATCGGGCAAACAAGTCAAGTGTCACTCTGGTTATGCTGG  
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGAAGCCCGGCCCTGTAAGCACAGGTGCATGAACACTTA  
CGGCAGCTACAAGTGTACTGTCACCGATATGCTCATGCCGGATGGTCTGCTCAAGTGCCTGACCTG  
CTCCATGGCAAACGTCAAGTATGGCTGTGATGTTAAAGGACAATACGGTGCAGTGCCTGACCTG  
GCACCTGGCTCTGATGGGAGGACCTGTAGATGTTGATGAATGTCTACAGGAAGAGCCTGCCCTAGATT  
TAGGCAATGTGTCAACACTTTGGGAGCTACATCTGCAAGTGTCAAAAGGCTTCGATCTCATGTATATTGGAGG  
CAAATATCAATGTGTCAACAGACGAATGCTCACTGGTCAGTATCAGTGCAGCAGCTTGCTCGATGTTATAA  
CGTACGTGGCTTACAAGTCAAATGTAAGAAGGATAACGGGTGATGGACTGACTTGTGTATATCCAAA  
AGTTATGATTGAAACCTTCAGGCTCAATTCTGACCAAAGGAAATGGTACCCATTAAAGGGTGACACAGGAAA  
TAATAATTGGATTCTGATGTTGGAAGTACTTGGTGGCCCTCGGAAGACACCATATTCCCTCTATCATTACCAA  
CAGGCCTACTCTAAAGCCAACAACAAGACCTACACCAAAGCCAACACCAATTCCCTACTCCACCAACCAACCC  
CCTGCCAACAGAGCTCAGAACACCTCTACCCACCTACACCCCAAAGGCCAACACGGACTGACAACATATAGC  
ACCAGCTGCCAGTACACCTCAGGAGGATTACAGTTGACAACAGGGTACAGACAGACCCCTCAGAAACCCAGG  
AGATGTGTTCAAGTGTCTGGTACACAGTGTAAATTGACCATGGACTTGTGGATGGATCAGGGAGAAAGACAA  
TGACTTGCACGGGAAACCAATCAGGGACCCAGCAGGTGGACAAATATCTGACAGTGTGGCAGCCAAGGCCAGG  
GGGAAAAGCTGCACGCTGGTGTACCTCTCGGCCCTCATGCATTAGGGACCTGTGCCTGTCATTAGGCA  
CAAGGTGACGGGGCTGCACTTGGCACACTCCAGGTGTTGTGAGAAAACACGGTGCACGGAGCAGCCCTGTG  
GGGAAGAAAATGGTGGCATGGCTGGAGGCAAACACAGATCACCTGGCAGGGGCTGACATCAAGAGCGAATCACA  
AAGATTATTAAGGGTTGGAAAAAAAGATCTATGATGGAAAATTAAAGGAACCTGGGATTATTGAGCCTGGAGAAG  
AGAAGACTGAGGGCAAACCATGATGGTTTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCACCAGCTG  
TTCTCCATATGCACTAAGAATAGAACAGAGGAAACTGGCTTAGACTAGAGTATAAGGGAGCATTTGGCAGG  
GGCCATTGTTAGAATACTTCATAAAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTTTCTAAAAAATTAGA  
TAAAAATTGCTTAAAGATGGTAAAGATGTTCTTACCAAGGAAAGTAACAAATTATAGAATTCCAAA  
AGATTTGTTGATCCTACTAGTAGTATGCACTGAAATCTTACAACTAAATAATTGGACAAGGCTTAATTAGG  
CATTCTCCCTCTTGACCTCTTAATGGAGAGGGATTGAAAGGGAAAGAGGCCACAAATGCTGAGCTCACTGAAATA  
TCTCTCCCTATGGCAATCTGCACTTAAAGAAAAAGGAAACTATTATTCCAAATGAGAGTATGATGGAC  
AGATATTGTTGATCTCAGTAATGTCCTAGTGTGGCGGTGGTTCAATGTTCTCATGGTAAAGGTATAAGCC  
TTTCATTGTTCAATGGATGATGTTCAAGATTTTTTTAAGAGATCCTCAAGGAACACAGTTCAGAGAG  
ATTTCATGGGTGCATTCTCTGCTGTGACAAGTTATCTGCTGCTGAGAAAGAGTGCCTGCC  
ACACCGGCAGACCTTCTCACCTCATCAGTATGATTGACTTCTCTTATCAATTGGACTCTCCAGGTTCCAC  
AGAACAGTAATATTTTGAAACAATAGGTACAATAGAACGGTCTCTGTCATTAACTGGTAAAGGCAGGGCTGG  
AGGGGAAAATAATCATTAAGCCTTGAGTAACGGCAGAAATATGGCTGTAGATCCATTAAATGGTTCATT  
TCCTTATGGTCAATAACTGCACAGTGAAGATGAAAGGGAAAATAATGAAAATTACTTTCGATGCCAA  
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTGTTATTATTTAATGTTT  
CTAAAATAAAAATGTTAGTGGTTTCCAAATGGCCTAATAAAAACAATTATTTGAAATAAAACACTGTTAGTAAT

## **FIGURE 110**

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCPQ  
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPC KHRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCSMANCQYGC DVVKGQIRCQCPSPGLHLAPDGRTCVDVDECATGRASCPFRQC  
VNTFGSYICKCHKGFDL MYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKC KEGYQG  
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNWIPDVGSTWWPPKTPYIPPIITNRP  
TSKPTRPTPKPTPIPTPPPPPPLPTELRTPLPPTT PERPTTGLTTA PAASTPPGGITVDN  
RVQTDPQKPRGDVFSVLVHSCNFDHGLCGWI REKNDLHWEPIRD PAGGQYLT VSAAKAPGG  
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGTLQFVRKHGAHGAALWGRNGGHGW RQQTQI  
TLRGADIKSESQR

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 273-277

**Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

**Tyrosine kinase phosphorylation site.**

amino acids 199-206

**N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482

**Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

**Cell attachment sequence.**

amino acids 382-385

**EGF-like domain cysteine pattern signature.**

amino acids 75-87

## **FIGURE 111**

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTGCCCTTAGATTGTGA  
**AATGTGGCTCAAGGTCTTCACAACCTTCCTTCCTTGCAACAGGTGCTGCTGGGGCTGA**  
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACCTACCGTC  
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCA  
ACAATGCCCAAATACTTACTGGCTCTGTGAATAAGTCTGTGGTCTGACTTGAATACC  
AACACAAGTTACCATGATGCCACCCAAATGCATCTGTCTTATCAACCCACTGCAGTCCCT  
GATGAAGGCAATTACATCGTGAAGGTCAACATTCAAGGAAATGGAACTCTATCTGCCAGTCA  
GAAGATACAAGTCACGGTGATGATCCTGTCACAAAGCCAGTGGTGCAGATTCATCCTCCCT  
CTGGGGCTGTGGAGTATGTGGGAACATGACCCCTGACATGCCATGTGGAAGGGGGACTCGG  
CTAGCTTACCAATGGCTAAAAAAATGGGAGACCTGTCCACACCAGCTCACCTACTCCTTTTC  
TCCCCAAAACAATACCCCTCATATTGCTCAGTAACCAAGGAAGACATTGGGAATTACAGCT  
GCCTGGTGAGGAACCCCTGTCAGTGAATGGAAAGTGATATCATTATGCCCATCATATTAT  
GGACCTTATGGACTTCAAGTGAATTCTGATAAAAGGCTAAAGTAGGGGAAGTGTAACTGT  
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT  
CCTGGATTAGGAGGAAGTACAATACTACATATATCATTAAGCATGGGCCCTCGCTTAGAAGTT  
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGCTTACAACAAACATAAC  
CGGCAGGCAAGATGAAACTCATTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTG  
CACAGAAAAGGAAAATCATTGTCACCTTAGCAAGTATACTGGAAATATCACTATTTTGATT  
ATATCCATGTGTTCTCTTCTCATGGAAAAAAATCAACCCCTACAAAGTTATAAAACAGAA  
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG  
CTCTGGATGACTTCGGAATATATGAATTGTTGCTTTCCAGATGTTCTGGTGTTCAGG  
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTTGCTGACAGTACAGT  
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGACCATCCAGAGT**GAAC**TTTCA  
GCTAAACAGTACATTCAAGTGAAATTCTGAAGAACATTAAAGGAAAACAGTGGAAAAGT  
ATATTAAATCTGGAATCACTGAAGAAACCAGGACCAACACCTCTTACTCATTATCCTTTACA  
TGCAGAAATAGAGGCATTATGCAAATTGAACTGCAGGTTTCAGCATATACACAATGTCTT  
GTGCAACAGAAAAACATGTTGGGAAATATTCCCTCAGTGGAGAGTCGTTCTCATGCTGACGG  
GGAGAACGAAAGTGACAGGGTTCCCTCATAAGTTGTTGATGAAATATCTCTACAAACCTCA  
ATTAGTTCACTCTACACTTCACTATCATCAACACTGAGACTATCCTGTCACCTACAAA  
TGTGGAAACTTACATTGTTGCTGATTTCAGCAGACTTGTGTTATTAAATTTTATTAGTG  
TTAAGAATGCTAAATTATGTTCAATTTCAGGAAATTCTATCTGTTATTGTACAA  
CAAAGTAATAAGGATGGTTGTCAACAAAACAAAATGCTTCTCTTTTCAATCACC  
AGTAGTATTGAGAAGACTTGTAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA  
TTTTTCAAGGAAAGATGGATTCAAATAATTATTCTGTTGCTTTAAAAAAA

## **FIGURE 112**

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGTLSASQ  
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS  
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV  
DLGEAILFDCSADSHPPNTYSWIRTDNTTYIIKHGPRLEVASEKVAQKTMVDYVCCAYNNIT  
GRQDETHFTVIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSPASDCVSGQDLHSTV  
YEVIQHIPAQQQDHPE

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 341-359

**N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

**Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

**Tyrosine kinase phosphorylation site.**

amino acids 272-280

**N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 113**

GCAAGCGCGAAATGGCGCCCTCCGGAGTCCTGCAGTCCTCCCTGGCAGTCCTGGTGTGTT  
GCTTGGGGTGCCTCCCTGGACGCACGGGGCGGAGCAACGTTGCGTCATCACGGACGAGA  
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCTGCT  
TGTCAAAAATCTCAACCGAATGGAAAGTTTGCTGAATGGGAGAAGATCTTGAGGTTAA  
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC  
TTCCTACTATTATCATTGTAAGATGGTGAATTAGGCCTATCAGGGTCCAAGGACTAAG  
AAGGACTTCATAAAACTTATAAGTGATAAAGAGTGGAGAGTATTGAGCCGTTCATCATG  
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA  
TCAGGACGTGCCATAACTACTTATTGAAGACCTTGGATTGCCAGTGTGGGATCATATACT  
GTTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC  
AGATTGCCCTTGTCTTCAAAAGGCGCAGACCACAGCCATACCCATACCCCTCAAAAAAAAT  
TATTATCAGAATCTGCACAACCTTGAAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA  
GATGTTCAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGC  
CATAAAGACAACGCTCTGGGTCCATCATTGCCACAGATAAATCCAGTTAAATTATAG  
TTATCTTAATATTATGATTTGATAAAACAGAAGATTGATCATTGTTGGTTGAAGTG  
AACTGTGACTTTTGAAATATTGCAAGGTTCACTCTAGATTGTCATTAAATTGAAGAGTCTA  
CATTGAGAACATAAAAGCACTAGGTATACAAGTTGAAATATGATTTAACAGTATGATG  
GTTTAAATAGTCTCTAATTTGAAAAACGTGCCAAGCAATAAGATTATGTATATTG  
TTAATAATAAACCTATTCAAGTCTGAGTTTGAAAATTACATTCCCAAGTATTGCAATTAT  
TGAGGTATTAAAGAAGATTATTAGAGAAAATATTCTCATTGATATAATTCTCTG  
TTTCACTGTGTGAAAAAAAGAAGATATTCCCATAAATGGGAAGTTGCCATTGTCTCAAG  
AAATGTGTATTCAAGTACAATTCTGGTCTTTAGAGGTATATTCAAATTTCTGT  
ATTTTAGGTTATGCAACTAATAAAACTACCTTACATTAAATTACAGTTCTACACA  
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTAAGTTCATGGTATTCTCTGATT  
CAACAAAGTTGATTTCTCTGTATTCTTACTATGGTTACATTTTATT  
CAAATTGGATGATAATTCTGGAAACATTTTATGTTTAGTAAACAGTATTCTGTT  
GTTTCAAACTGAAGTTACTGAGAGATCCATCAAATTGAACAACTGTTGAATTAAAATT  
TTGGCCACTTTTCAGATTTCATCATTCTGCTGAACTCAACTGAAATTGTTTTT  
TTTCTTTGGATGTGAAGGTGAACATTCTGATTGGTCTGATGTGAAAAAGCCTGGTA  
TTTACATTGAAAATTCAAAGAAGCTTAATATAAAAGTTGCATTCTACTCAGGAAAAG  
CATCTCTGTATATGCTTAAATGTATTGGTCTCATATAACAGAAAGTTCTTAATTGAT  
TTTACAGTCTGTAATGCTGATGTTAAAATAACATTATTATTTAAAAGACAA  
ACTTCATATTATCCTGTTCTTCTGACTGGTAATATTGTGTGGGATTTCACAGGAAAA  
GTCAGTAGGATGGAACATTAGTGTATTCTACTCCTTAAAGAGCTAGAATACATAGTTT  
CACCTTAAAGAAGGGGGAAAATCATAAATACAATGAATCAACTGACCATTACGTAGAC  
AATTCTGTAATGTCCCTTCTTAGGCTCTGTTGCTGTGAATCCATTAGATTACAG  
TATCGTAATATACAAGTTCTTAAAGCCCTCTCCTTAAAGTAAATTTAAAATATTGTACCATT  
AAAGAGTTGGATGTGTAACTTGTGATGCCTAGAAAAATACCTAACGACAAAATAACCT  
TTCTAACCAACTCATTAAAGCTGAAAAAA

## FIGURE 114

MAPSGSLAVPLAVLVLLLWGPWTHGRRSNVRVITDENWRELLEGDWMIIFYAPWCPACQNL  
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI  
NFISDKEWKSIEPVSSWFGPGSVMSSMSALFQLSMWIRTCNYFIEDLGLPVWGSYTVFAL  
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE  
EEAESKEGTNKDFPQNAIRQRSLGPLATDKS

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 182-201

**Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

**Tyrosine kinase phosphorylation site.**

amino acids 107-115

**N-myristoylation site.**

amino acids 20-26, 192-198

**Amidation site.**

amino acids 25-29

## **FIGURE 115**

GCGAGTGTCCAGCTGCCAGACCCGTGATAATTGTTAACTAATTCAACAAACGGGACCCCTT  
CTGTGTGCCAGAAACCGCAAGCAGTGTGCTAACCCAGTGGGACAGGCCGATTGGAAGAGCGGG  
AAGGTCTGGCCCAGAGCAGTGTGACACTTCCCTGTGACCATGAAACTCTGGGTGCTGC  
ATTGCTGATGGCCTGGTTGGTGTCTGAGCTGTGCAGGCCGAATTCTCACCTCTATTG  
GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTGTAAAGAGTACATC  
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGCCAACAAAATGGAAGCCTTGAC  
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG  
TGAACGGCTAACACACAGACTGGCCTGCCGGAGGACCTTGTCCCTGCAGGACTCAGCTGCA  
GGTTTATGCCAACCTCTGTGCAGCGCAGTCTTCCCCACTGATGAGGACGAGATAGG  
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA  
GAGGGAACTTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG  
GGCGCTCGGCTACAATGAAGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT  
AAAGCAGCTTGATGCCGGGAGGAGGCCACACAAACCAAGTCACAGGTGCTGGACTACCTCA  
GCTATGCTGCTTCCAGTTGGGTGATCTGCACCGTGCCTGGAGCTCACCGCCGCTGCTC  
TCCCTGACCCAAAGCCACGAACGAGCTGGAGGGATCTGCCGTACTTTGAGCAGTTATTGGA  
GGAAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAGGCA  
TCTATGAGAGGCCCTGTGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTCTGCGTGGG  
GAGGGTGTCAAACGTACACCCCGTAGACAGAAGAGGCTTTCTGTAGGTACCAACATGGCAA  
CAGGGCCCCACAGCTGCTCATTGCCCTTCAAAGAGGAGGACGAGTGGACAGCCGACA  
TCGTCAGGTACTACGATGTCATGCTGATGAGGAATCGAGAGGATCAAGGAGATCGCAAAA  
CCTAAACTTGACGAGCCACCGTCTGATCCAAGACAGGAGTCCTCACTGCGCCAGCTA  
CCGGTTTCCAAAGCTCCTGGTAGAGGAAGATGATGACCCCTGTTGGCCGAGTAAATC  
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGAGCAATTGTTACAGGTTGCAAAT  
TATGGAGTGGGAGGACAGTATGAACCGCACTCGACTTCTAGGCAACCTTTGACAGCGG  
CCTCAAAACAGAGGGAAATAGTTAGCGACGTTCTTAACATACATGAGTGTAGAAGCTG  
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAACAGAGGATACAGCTGTG  
TTCTGGTACAACCTCTTGCAGCGGGGAAGGTGACTACCGAACAGACATGCTGCCTGCC  
TGTGCTTGTGGCTGCAAGTGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT  
TGAGACCTTGTGGATCAACAGAAGTTGACTGACATCCTTCTGTCCTCCCTTCTGGTC  
CTTCAGCCCCATGTCAACGTGACAGACACCCCTGTATGTTCTTGTATGTTCTATCAGGCT  
GATTTTGGAGAAATGAATGTTGTCAGGAGCAGAGGGAGACCAACTAGGGCACTCTGT  
GTGACTGAAGTCCCAGCCCTCCATTCAAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA  
AAAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTGTACCTCAGGTGTT  
TTAGGTGTGAGATGTTCAAGTGAACCAAAGTTCTGATACCTGTTACATGTTGTTTAT  
GGCATTCTATCTATTGTGGTTACCAAAAAATAAAATGTCCTACCAAGAAAAAAA

## **FIGURE 116**

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLDQDSAAGFIANLSVQRQFFP  
TDEDEIGAAKALMRLQDTYRLDPGTISRGEGLPGTKYQAMLSVDDCFGMGRSAYNEGDYHTV  
LWMEQVLKQLDAGEEATTKSQVLDYLSYAVFQLGDLHRALELTRRLLSLDPSHERAGGNLR  
YFEQLLEEREKTLTNQTEAELATPEGIYERPVDPYLPERDVYESLCRGEVVKLTPRRQKRLF  
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYDVMSDEEIERIKEIAKPKLARATVRDPKTG  
VLTVASYRVSKSSWLEEDDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHDFD  
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEVDYR  
TRHAACPVLVGCKWVSNKFHERGQEFLRPCGSTEVD

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 115-119, 264-268

**Glycosaminoglycan attachment site.**

amino acids 490-494

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

**Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

**N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

**Leucine zipper pattern.**

amino acids 213-235

## **FIGURE 117**

GCAGTATTGAGTTTACTTCCCTCTTTAGTGGAAAGACAGACCATAATCCCAGTGTGAGTGAAATTGATTGT  
TTCATTATTACCGTTTGGCTGGGGTTAGTCCGACACCTCACAGTGTGAAAGAGCAGGCAGAAGGAGTTGTGA  
AGACAGGACAATCTTCTGGGGATGCTGGTCCTGGAAGGCCAGGGCCTGCTCTGCTTTGGCCTCATTGACCC  
CAGGTTCTGGTTAAACTGAAAGCCTACTACTGGCCTGGTCCCCATCAATCATTGATCCTTGAGGCTGTGCC  
CCTGGGCACCCACCTGGCAGGGCCTACCACCATGCGACTGAGCTCCCTGTTGGCTCTGTCGGCCAGGCCCTC  
CCCTCATCTTAGGGCTGTCTCTGGGTGAGCCTGAGCCTCTGCGGGTTCTGGATCCAGGGGAGGGAGAAG  
ATCCCTGTGTCGAGGCTGTAGGGGAGCAGGAGGCCACAGAATCCAGATTGAGAGCTGGCTAGACCAAAGTG  
ATGAAGACTTCAAACCCCGATTGTCCCCTACTACAGGGACCCAAACAAGCCCTACAAGAAGGTGCTCAGGACTC  
GGTACATCCAGACAGAGCTGGCTCCCGTGAGCGGTTGCTGGCTGTGACCTCCCGAGCTACACTGTCCA  
CTTGGCCGTGGCTGTGAAACCGTACGGTGGCCCATCCTCCCTCGGTTACTCTACTTCAGTGGCAGCGGGGG  
CCCGGGCTCCAGCAGGGATGCAAGGTGGTGTCTCATGGGATGAGCGGCCGCGCTGGCTCATGTCAGAGACCCCTGC  
GCCACCTTCACACACACTTGGGGCCGACTACGACTGGTTCTCATCATGCAAGGATGACACATATGTGCAAGGCC  
CCCGCCTGGCAGCCCTTGCTGGCCACCTCAGCATCAACCAAGACCTGACTTGGCCGGCAGAGGAGTTCATGG  
GCGCAGCGAGCAGGCCGGTACTGTCTGGCATGGGGCTTGGCTACCTGTTGTCACGGAGTCTCCTGCTCTGC  
GGCCACATCTGGATGGCTGCGCAGGGAGACATTCTCAGTGGCCCTCTGACGAGTGGCTGGACGCTGCCTCATGG  
ACTCTCTGGCGTCGGCTGTGTCACAGCACCAGGGCAGCAGTATCGTCATTTGAACGGCCAAAATAGGG  
ACCCCTGAGAAGGAAGGGAGCTCGGCTTCTGAGTGCCTTCGGCTGACCCCTGTCCTCGAAGGTACCCCTCATGT  
ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGCGGGTTACAGTGAACATAGAACAACTGCAGGCTCAGA  
TCCGGAACCTGACCGTGCTGACCCCGAAGGGGAGGAGGGCTGAGCTGGCCGTTGGCTCCCTGCTCCTTCA  
CACCACACTCTCGCTTGAGGTGCTGGGACTACTTCACAGAGCAGCACACCTCTCTGTGCAAGATGGGG  
CTCCCAAGTGGCCACTACAGGGGGTAGCAGGGCGACGTGGGTATGCGTTGGAGACTGCCCTGGAGCAGCTCA  
ATCGGGCCTATCAGCCCCGCGCTTCCAGAAGCAGCGACTGCTCAACGGCTATCGCGCTTCGACCCAGCAC  
GGGGCATGGAGTAACCCCTGGACCTGCTGTTGGAAATGTGTGACACAGCGTGGCACCGGCGGGGCTGGCTCGCA  
GGGTAGCCTGCTGCGGCCACTGAGCCGGTGGAAATCCTACCTATGCCCTATGTCACTGAGGCCACCCGAGTGC  
AGCTGGTGCTGCCACTCTGGTGCTGAAGCTGCTGAGCCGGCTTCCCTGAGGCCATGTCCAG  
TGGAGCCACGAGAACATGCTACCCCTGTTGCTGGTCTACGGGCCAGAGAAGGTGGCGTGGAGCTCCAG  
ACCCATTCTGGGGTGAAGGCTGAGCAGCGGAGTTAGAGCAGCGTACCCCTGGAGGCTGGCTGGCTCG  
CTGTGCGAGCAGAGGCCCTTCCAGGTGCACTCATGGACGTGGCTCGAAGAACGACCCCTGTGGACACTCTCT  
TCTTCCCTTACCAACCGTGTGGACAAGGCCCTGGCCGAAGTCCCAACCGCTGTCGATGAATGCCATCTGGCT  
GGCAGGCCCTTCCAGTCCATTCCAGGAGTTCAATCCTGCCCTGTCACCACAGAGATCACCCCAAGGCC  
CGGGGGCTGGCCCTGACCCCCCTCCCTGGTCTGACCCCTCCCGGGGGCTCTATAGGGGGAGATTG  
ACCGGCAGGCTCTGCGGAGGGCTGCTTCTACAACGCTGACTACCTGGCGGCCAGGCCGGCTGGCAGGTGAAC  
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGCTGGTGCAGAAGTTCTCCCTGCGAGACTGCAGCCCACGGCTCAGTGAAG  
ACCTCTTCTGGCCGTAGAGCCAGGGCTGGTGCAGAAGTTCTCCCTGCGAGACTGCAGCCCACGGCTCAGTGAAG  
AACTCTACCAACCGCTGCCCTCAGCAACCTGGAGGGCTAGGGGCCGTGCCAGTGGCTATGGCTCTTTG  
AGCAGGAGCAGGCCAATAGCACTTAGCCCGCTGGGGCCCTAACCTCATTACCTTGTCTGCCCTAGCC  
CCAGGAAGGGCAAGGCAAGATGGTGACAGATAGAGAATTGTTGCTGTATTTTAAATATGAAAATGTTATTAA  
ACATGCTTCTGCC

## **FIGURE 118**

MRLSSILLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPD  
SARLDQSDEDFKPRIVPYYRDPNKPYKKVLRTRYIQTELGSRERLLVAVLTSRATLSTLAVAVNRTV  
AHHFPRLLYFTGQRGARAPAGMQVVSQHDERPAWLMSETLRHLHFGADYDWFFIMQDDTY  
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLRPHLDGC  
RGDILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE  
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTP  
HSRFEVLGWDYFTEQHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRYQPR  
LRFQKQRLLMGYRRFDPARGMNEYTL DLLECVTQRGHRRALARRVSLLRPLSRVEIL  
PMPYVTEATRVQLVLPPLLVAEAAAAPAFLEAFAANVLEPREHALLTL  
LVYGPREGGRGAPDPFLGVKAAAELERRYPGTRLAWLAVRAEAPS  
QVRLMDVVSKKHPVDTLFFLTTVWTRPGPEVLMRCRMNAISGWQAFFPVHFQE  
FPNPA  
LSPQRSPGPPGAGPDPPSPGADPSRGAPIGGRFD  
RQASAEGCFYNADYLAA  
RARLAGELAGQEEE  
EALEGLEVM  
DVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHRCRLSN  
LEGLGGR  
AQLAMALFEQE  
QANST

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 489-507

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## **FIGURE 119**

CGGAGTGGTGC~~CG~~CAACGTGAGAGGAACCGTGC~~CG~~CGCTGCCTTCCTGTCCCCAAGCC  
GTTCTAGACG~~CG~~GGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTATGCTTGG  
AAGCATTCTGTGCTTGTACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTGAAAATTCA  
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC  
CAAAGATGTGAGTCTTGGGCTGCAGTAAAGGAGACTGGACAAACACTGTGACAAAGCAG  
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCATTAATATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTGATAAGTATAAGGACCAATACAAC  
GTTCTCCTGCACGCCACTACGTTGCTATGAAAACCTAAAGTATTTTTGTTAA  
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT  
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTCT  
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC  
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCAGAAAATGCAGAAGATGCTGATGGA  
AAAGATGTATTTAACCAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC  
CAACCAGGTAGTAGAAGGCTGTTGTCAGATATGGCTGTTACTTTAATGGACTGACTCCAA  
ATCAGATGCATGTGATGATGTATGGGTATACGCCCTAGGGCATTGGCATATTTCAAT  
GATGCATTGGTTTCTTACCTCCAAATGGTCTGACAATGACTGAGAAGTGGTAGAAAAGCG  
TGAATATGATCTTGTATAGGACGTGTGTCATTATTTGTAGTAGTAACATACATATCCAA  
TACAGCTGTATGTTCTTTCTTCTAATTGGTGGCACTGGTATAACCACACATTAAAG  
TCAGTAGTACATTTAAATGAGGGGGTTTTCTTAAAACACATGAACATTGAAATG  
TGTTGGAAAGAAGTGTGTTAAGAATAATAATTGCAAATAACTATTAATAATATTAT  
GTGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGCACATATTTGCTGATTGGTT  
AAAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT  
TGTGATTAAGTAAAACCTTGTGTTCCCTTACTCTAATACTGATTTATGTTCT  
AAGCCTCCCCAAGTTCCAATGGATTTGCCTCTCAAATGTACAACTAAGCAACTAAAGAAA  
ATTAAGTGAAGTGGAAAAT

## **FIGURE 120**

MLSSESSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME  
LSKSFRVYCIILVKPKDVSLLAAVKETWTKHCDKAFFSSENVKFESINMDTNDMWLMMRK  
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG  
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT  
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL  
PPNGSDND

**Signal sequence:**

amino acids 1-33

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## **FIGURE 121**

CCACCGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG  
AAAAAGAGAGAGAGAGAAACAAAAACCAAAGAGAGAGAAAAATGAATTCATCTAAATCAT  
CTGAAACACAATGCACAGAGAGAGGATGCTCTCTCCAAATGTTCTTATGGACTGTTGCT  
GGGATCCCCATCCTATTCTCAGTGCCTGTTCATCACCAGATGTGTTGACATTTCGCAT  
CTTTCAAACCTGTGATGAGAAAAAGTTCAGCTACCTGAGAATTACAGAGCTCTCCTGCT  
ACAATTATGGATCAGGTTCAAGAATTGTTGTCATTGAACGGAAATTTCACAGAGCTCAGC  
AGCTGCTACTCTTTCTACTGACACCATTCCCTGGCGTTAAGTTAAAGAACTGCTCAGC  
CATGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCCTTACAAAGA  
AACCTAAAATGAGAGAGAGTTTTATTGGACTGTCAGACCAGGTTGTCAGGGTCAGTGGCAA  
TGGGTGGACGGCACACCTTGACAAAGTCTCTGAGCTCTGGATGTAGGGAGGCCAACAA  
CATAGCTACCCCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGCAAATTGGA  
ATGATGTAACCTGTTCTCAATTATTTGGATTGTGAAATGGTAGGAATAATCCTTG  
AACAAAGGAAAATCTCTTAAGAACAGAAGGCACAACCAAATGTGAAAGAAGGAAGAGCA  
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTGTGCGCTGAACCTCAAAGGACTTC  
ATAAGTATTGTTACTCTGATAAAATAAGTAGTTAAATGTTAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAA  
AAAAAA

## **FIGURE 122**

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN  
FTELSCYNYGSGSVKNCCPLNWEYFQSSCYFFSTDТИWALSLKNCSAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNNIATLEDCATMRDSS  
NPRQNWNNDVTCFLNYFRICEMVGINPLNKGKSL

**Signal sequence:**

amino acids 1-42

**N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

**Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

**N-myristylation site.**

amino acids 15-21, 74-80, 155-161

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

## **FIGURE 123**

GGGACTACAAGCCGCGCCCGCTGCCGCTGGCCCCCTCAGCAACCCTGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCTGCTGCTGCTTTCAAGGGGCTGCCTGATAGGGCTGTAAATC  
TCAAATCCAGCAATCGAACCCCCAGTGGTACAGGAATTGAAAGTGTGGAACATGTGCTGCATCATTACGGATTGCG  
AGACAAGTGACCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACACATATGTGTTTTGACAACAAAAA  
TTCAGGGAGACTTGGCGGGCTCGCAGAAAATCTGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG  
ACTCAGCCCTTATCGCTGTGAGGTGCTGCAAATGACCGAAGGAAATTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGAACCTGCTGTAGAGTGCCTGAAGGCTGTACAGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGAGTGGAGGGCCACCCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT  
CCAGAGCCAATCCCAGATTGCAATTCTCTTCACTTAAACTCTGAAACAGGCACCTTGGTGTACTGCTG  
TTCACAAGGACGACTCTGGCAGTACTACTGCATTGCTTCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG  
AGATGAAAGTCTATGACCTGAAACATTGGCGAATTATTGGGGGGTCTGGTGTCTGCTGTACTGCCCTGA  
TCACGTTGGGCATCTGCTGTGCATACAGCTGGTACTTCATCAACAAATAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAAACCAAGATGGAGTTAACATCCGCACTGACGAGGAGGGCAGTCAGACACAAAGTCATCGTTG  
TGATCTCGAGACCCCGGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA  
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTGAGAAGCTTTGGCCAAAGTGTGACCA  
CTACTCTCTTACTCTAACAGGCCACATGAATAGAAGAATTTCCTCAAGATGGACCCGGTAATATAACCA  
GGAAGCGAACACTGGTGGCTTACTGAGATTGGTCTTAATCTGTTCTGGCCTGATTCGGCAGTGGATTAGG  
GTGATCTAAAGAGTTGCTCACGTAACGCCGTGCTGGGGCTGTGAAGCCAGCAGTGTACCACTGGTCGT  
CAGCAGCCACGACAGCAGCATGTGAGATGGCGAGGTGGCTGACAGCACCAGCAGCCATCCGGCGGGAACCA  
GAAAAGGCTTCTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTCTTCTAAAGGCTCTGC  
TGATCGGTGTTGAGTGTCCATTGAGAAGCTTTGGATCAGCATTGAAACAAACAAACAAATCAGGAAG  
GTAAATTGGTGTGGAAGAGGGATCTGCTGAGGAACCCCTGTTGCTCAACAGGGTGTCAAGGATTTAAGGAAA  
ACCTTCGTCTTAGGCTAACGACTGAAATGGTACTGAAATATGCTTTCTATGGTCTGTGTTATTTATAAAATT  
TACATCTAAATTGGTAAAGGATGTATTTGATTGAAAAGAAAATTCTATTAAACTGAAATATATTGT  
CATACATGTTAAATAACCTATTGTTAAAAAGTCAACTTAAGGTAGAAGTCCAAAGCTACTAGTGTAAAT  
TGGAAAATATCAATAATTAGTATTGTTACCAAGGAATCCTCATGGAAGTTACTGTGATGTTCTTTCT  
CACACAAGTTTACGCTTTTCAAGGAAACTCATACTGCTACACATCAGACCATAGTTGCTTAGGAACCTT  
TAAAATCCAGTTAACGAAATGTTGAAATCAGTTGCTCTCTCAAAGAAACCTCTCAGGTAGCTTTGA  
GCCTCTCCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGGCCCTCAGATGTACATACACAGATG  
CCAGTCAGCTCTGGGGTTCGGCCAGGGCGCCCCCTCTAGCTCAGTGTGCTCGTGTCCAGGAGGCCCT  
GCCATCCTGGGGCTGGCAGTGGCTGTGCTCCAGTGCAGTGGCTCCATGAGCTTCTGCTCATCCAGCACAGC  
TCTCAGGTGGGCAGTGCAGGGACACTGGTGTCTTCAATGAGCTCCAGTGTGCTCTGTAACAGACCTCT  
TTTGTTATGGATGGCTCACAAAATAGGGCCCCAATGCTATTGTTTTAAGTTGTTAATTATTGTT  
AAGATTGCTAACGCCAACAGCAATTGCGAAATCAAGTGTCAAGTACAATAACATTGTTAAAGAAAATGGAT  
CCCACGTGTTCTCTTGCCACAGAGAACGACCCAGCAGCCACAGGCTCTGCGATTTCAAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAGGGCTGGGGGGAGGAAAG  
TGAAACGCCGTGAATCAAAGCAGTTCTAATTGACTTTAATTTCATCCGCCAGACACTGCTCCATT  
TGTGGGGGACATTAGCAACATCACTCAGAAGCTGTGTTCTCAAGAGCAGGTGTCTCAGCCTCACATGCCCT  
GCCGTGCTGGACTCAGGACTGAAGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCAGTCCACTGTGCTGG  
GAATGGCTCTCACTACTCACCTTGCTTCACTGCTCCAGTGTCTGGTTTTATACTTTGACAGCTTTTT  
AATTGCTACATGAGACTGTGTTGACTTTTTAGTTATGAAACACTTGCGCAGGCGCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGCCTCTGGTGTCTGCTGCATGGCATTCTGGATGCTTAGCATGCAAGTTC  
CCTCCATCATGCCACCTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCGTGGGGATTACCGCTCCAGGCC  
TCTTGGTTGTCTAGTGTAGGGTAGGCTTATTGGCCCCCTCTTCTATACCCCTAAACCTCTACACTAGTGC  
TGGGAACCCAGGTCTGAAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCTTAAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGTATTGTTAAAGATATGAATGTGACTCAAGACTCGAGGCCAGACAGGGCTGTGATTCT  
GCCTTGGATGGATGGTGTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAAC  
CTCATTTATAAAAGCTCAAAAAACCA

## **FIGURE 124**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFLRLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEKKIQDQEQTYYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGIICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267